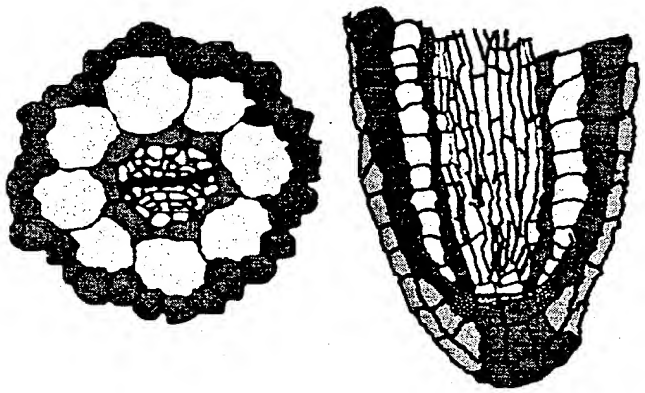


EPIDERMIS
CORTEX
ENDODERMIS
PERICYCLE
ROOT CAP
VASCULAR TISSUE
CORTEX/ENDODERMAL INITIAL
EPIDERMAL/ROOT CAP INITIAL
QUIESCENT CENTER

FIG. 1A

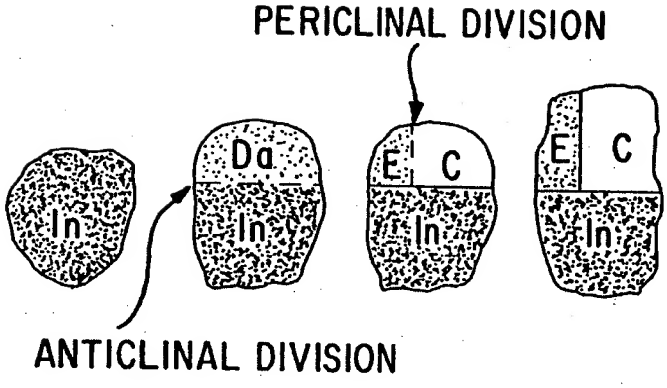


FIG. 1B

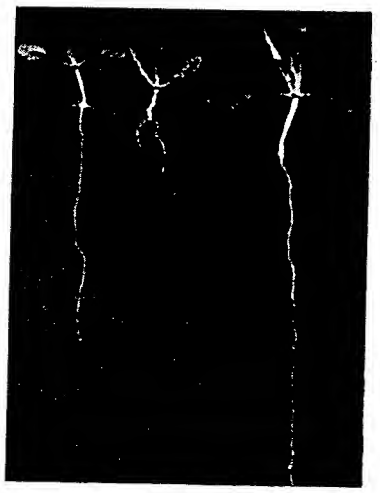


FIG.2A

FIG.2B

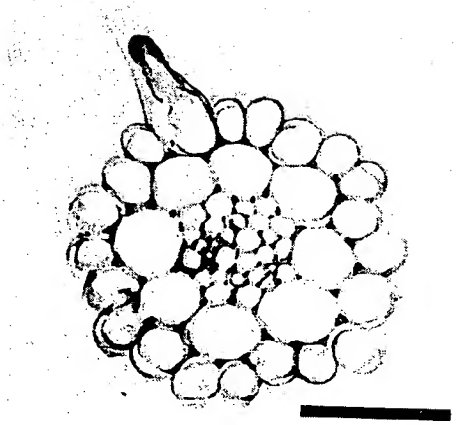


FIG.2C

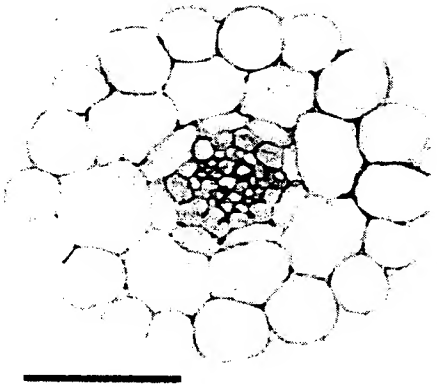


FIG.2D

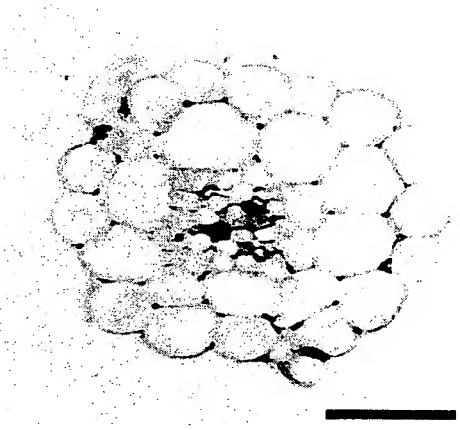


FIG.2E

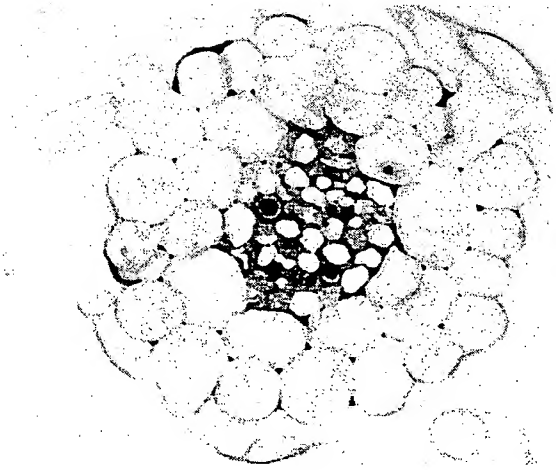


FIG.2F

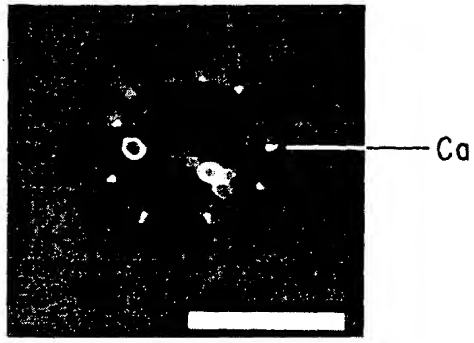


FIG.3A

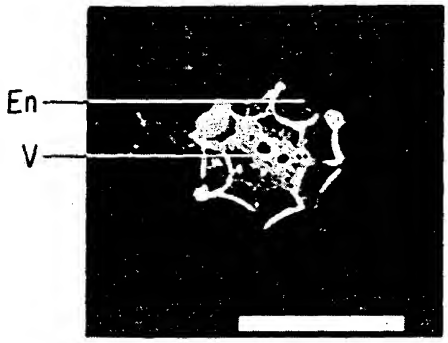


FIG.3D

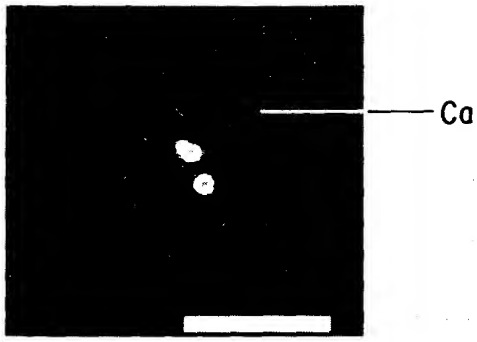


FIG.3B

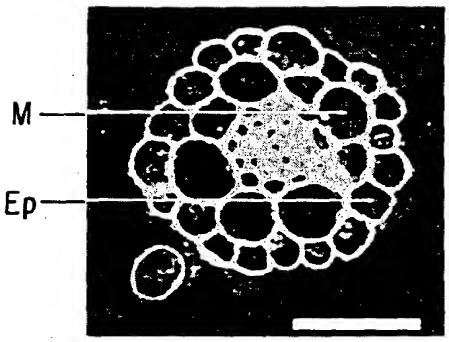


FIG.3E

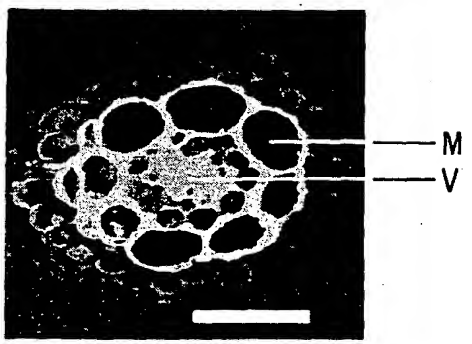


FIG.3C

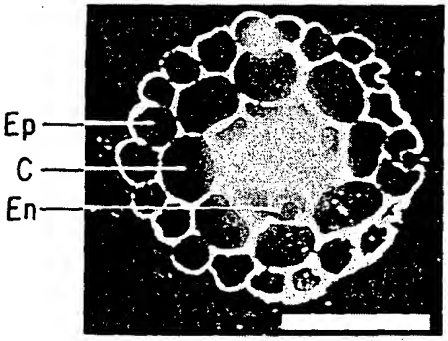


FIG.3F

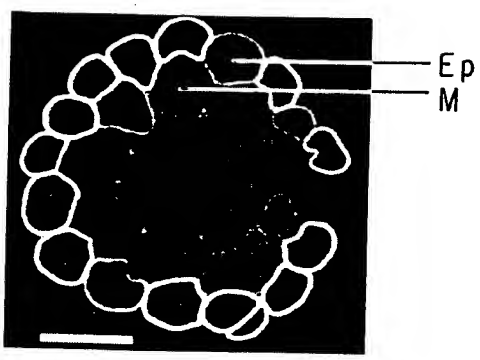


FIG.4A

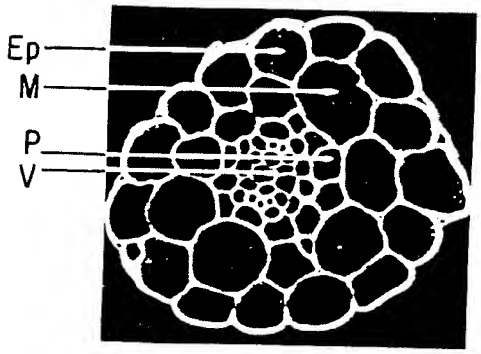


FIG.4D

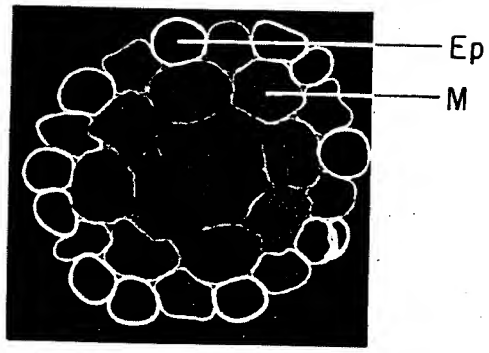


FIG.4B

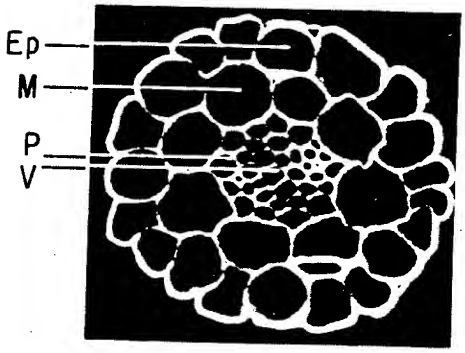


FIG.4E

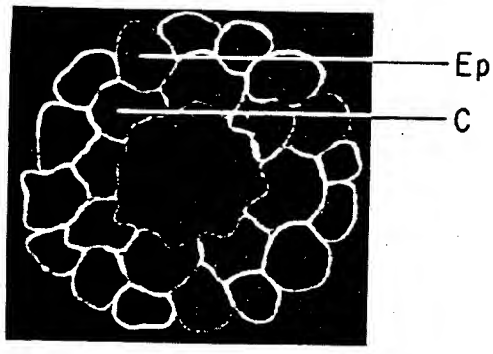


FIG.4C

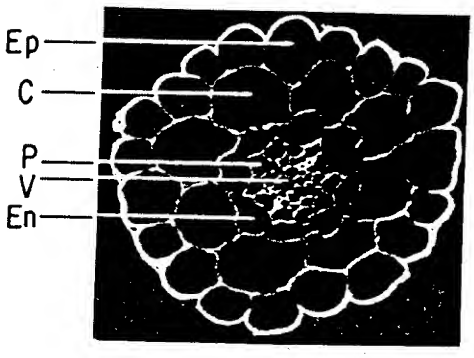


FIG.4F

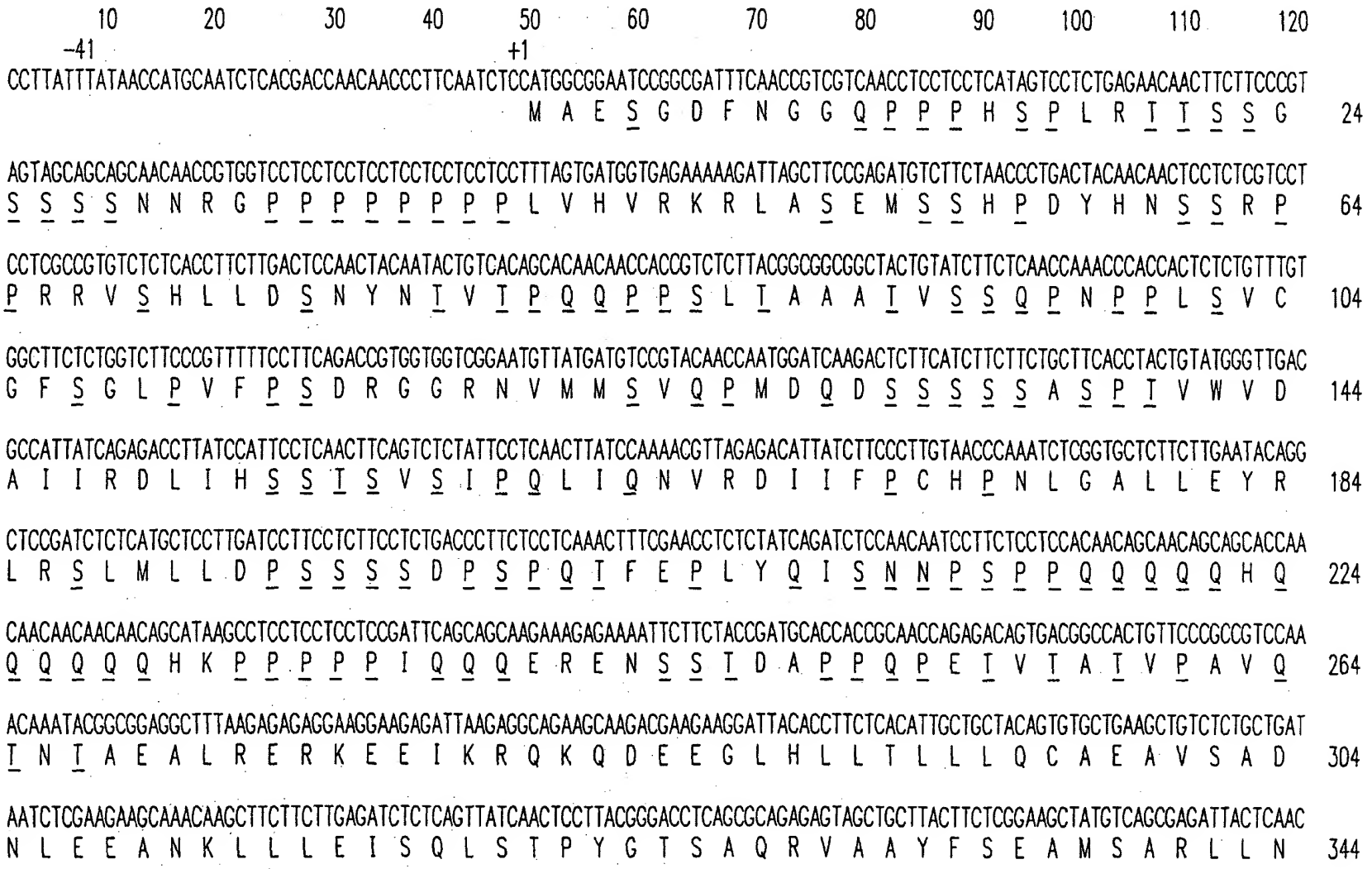


FIG.5A-1

```
TCGTGTCTCGGAATTTACGCGGCTTTGCCTTCACGGTGGATGCCTCAAACGCATAGCTTGAAAATGGTCTCTGCGTTTCAGGTCTTTAATGGGATAAGCCCTTTAGTGAAATTCTCACAC
S  C  L  G  I  Y  A  A  L  P  S  R  W  M  P  Q  T  H  S  L  K  M  V  S  A  F  Q  V  F  N  G  I  S  P  L  V  K  F  S  H   384

TTTACAGCGAATCAGGCGATTCAAGAAGCATTTGAGAAAGAAGACAGTGTACACATCATTGACTTGGACATCATGCAGCGACTTCAATGGCCTGGTTTATTCCACATTCTTGCTTCTAGA
F  T  A  N  Q  A  I  Q  E  A  F  E  K  E  D  S  V  H  I  I  D  L  D  I  M  Q  G  L  Q  W  P  G  L  F  H  I  L  A  S  R   424

CCTGGAGGACCTCCACACGTGCGACTCACGGGACTTGGTACTTCCATGGAAGCTCTTCAGGCTACAGCGAAACGTCTTTCGGATTTCACAGATAAGCTTCCCCTGCCTTTTGAGTTCTGC
P  G  G  P  P  H  V  R  L  T  G  L  G  T  S  M  E  A  L  Q  A  T  G  K  R  L  S  D  F  T  D  K  L  G  L  P  F  E  F  C   464

CCTTTAGCTGAGAAAGTTGGAAACTTGGACACTGAGAGACTCAATGTGAGGAAAAGGGAAGCTGTGGCTGTTCACTGGCTTCAACATTCTCTTTATGATGTCACTGCCTCTGATGCACAC
P  L  A  E  K  V  G  N  L  D  T  E  R  L  N  V  R  K  R  E  A  V  A  V  H  W  L  Q  H  S  L  Y  D  V  T  G  S  D  A  M   504

ACTCTCTGGTTACTCCAAAGGTAAAATAAACATTACCTTTTAATCACTCTTTATCTATAAATTATTTTAAGATTATATAGGAAAGATATGTTCTAAAAAGCTGGCTTTTTTCGTTAATGA
T  L  W  L  L  Q  R                                                                                                        511

TTCGGGAATGAACAGATTAGCTCCTAAAGTTGTGACAGTAGTGGAGCAAGATTTGAGCCACGCTGGTTCTTTCTTAGGAAGATTTGTAGAGGCAATACATTACTACTCTGCACTCTTTGA
                L  A  P  K  V  V  T  V  V  E  Q  D  L  S  H  A  G  S  F  L  G  R  F  V  E  A  I  H  Y  Y  S  A  L  F  D   546

CTCACTGGGAGCAAGCTACGGCGAAGAGAGTGAAGAGAGACATGTCGTCGAACAGCAGCTATTATCGAAAGAGATACGGAATGTATTAGCGGTTGGAGGACCATCGAGAAGCGGTGAAGT
S  L  G  A  S  Y  G  E  E  S  E  E  R  H  V  V  E  Q  Q  L  L  S  K  E  I  R  N  V  L  A  V  G  G  P  S  R  S  G  E  V   586

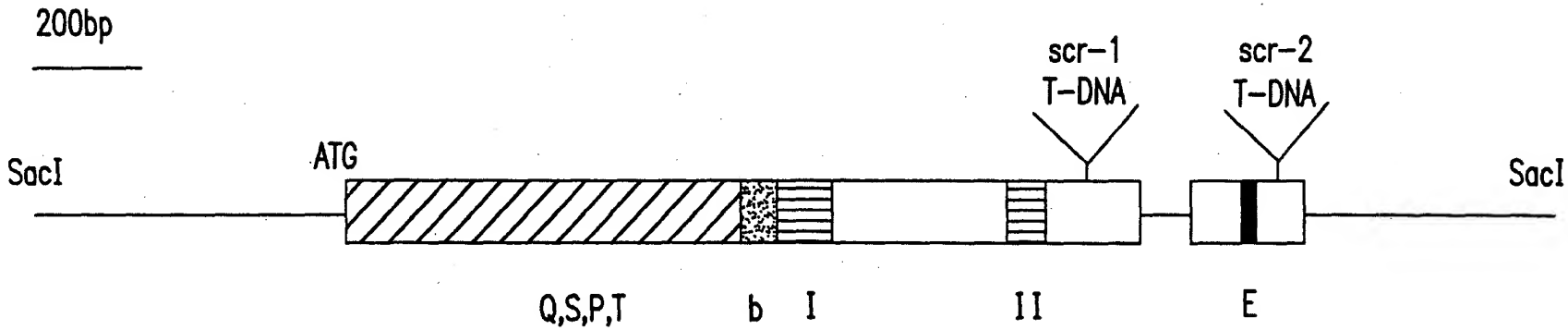
GAAGTTTGAGAGCTGCAGGGAGAAAATGCAACAATGTGGGTTTAAAGGTATATCTTTAGCTGGAAATGCAGCTACACAAGGGACTCTACTGTTGGGAATGTTTCCTTCGGATGGTTACAC
K  F  E  S  W  R  E  K  M  Q  Q  C  G  F  K  G  I  S  L  A  G  N  A  A  T  Q  A  T  L  L  L  G  H  F  P  S  D  G  Y  T   626

TTTGGTTGATGATAATGGTACACTTAAGCTTGGATGGAAAGATCTTTCGTTACTCACTGCTTCAGCTTGGACGCCTCGTTCTTAGTTTTCTTCTCCTTTTTCACAAACAATGTGCCCATA
L  V  D  D  N  G  T  L  K  L  G  W  K  D  L  S  L  L  T  A  S  A  W  T  P  R  S  STOP                                   653

2163
AAT
```

8/100

FIG.5A-2



PROBE

a

b

FIG.5B

			1
SCR bZIP-like domain		PAVQTNTAEALRERKEEIKRQKQ	D
		|| | | | : | ||	
GCN4	(yeast)	LKRARNTEAARRSRARKLQRMKQ	L
TGA1	(Arabidopsis)	RRLAQNREAARKSRLRKKAYVQQ	L
C-Fos	(mouse)	IRRERNKMAAAKCRNRRRELTDT	L
c-JUN	(human)	RKRMRNRIAASKCRKRKLERIAR	L
CREB	(human)	VRLMKNREAARECRRKKKEYVKC	L
Opaque-2	(maize)	KRKESNRESARRSRYRKAAHLKE	L
OBF2	(maize)	MRQIRNRDSAMKSRERKKSYIKD	L
RAF-1	(rice)	RRMVSNRESARRSRKKKQAHLAD	L

FIG.5C

SCR VHIID domain

```
                                                                  1
SCR         AFEKEDSVHIIDLDIMQGLQWPGLFHILASRPGGPPHVRLTGL
F13896      AVKNESFVHIIDFQISQGGQWVSLIRALGARPGGPPNVRITGI
Z37192      AMEGEKMVHVIDLDASEPAQWLALLQAFNSRPEGPPHLRITGV
Z25645      AIKGEEEVHIIDFDINQGNQYMTLIRSIA
D41474            IHVIDFXLGVGGQWASFLQELAHRRG
T18310            VHIIXFXLMQGLQWPALMDVFSARKGGPPKLRITGI
```

FIG. 5D

MetAlaGluSerGlyAspPheAsnGlyGlyGlnProProProHisSerProLeuArgThr

ThrSerSerGlySerSerSerSerAsnAsnArgGlyProProProProProProProPro

LeuValMetValArgLysArgLeuAlaSerGluMetSerSerAsnProAspTyrAsnAsn

SerSerArgProProArgArgValSerHisLeuLeuAspSerAsnTyrAsnThrValThr

ProGlnGlnProProSerLeuThrAlaAlaAlaThrValSerSerGlnProAsnProPro

LeuSerValCysGlyPheSerGlyLeuProValPheProSerAspArgGlyGlyArgAsn

ValMetMetSerValGlnProMetAspGlnAspSerSerSerSerSerAlaSerProThr

ValTrpValAspAlaIleIleArgAspLeuIleHisSerSerThrSerValSerIlePro

GlnLeuIleGlnAsnValArgAspIleIlePheProCysAsnProAsnLeuGlyAlaLeu

LeuGluTyrArgLeuArgSerLeuMetLeuLeuAspProSerSerSerSerAspProSer

ProGlnThrPheGluProLeuTyrGlnIleSerAsnAsnProSerProProGlnGlnGln

GlnGlnHisGlnGlnGlnGlnGlnGlnHisLysProProProProProIleGlnGlnGln

GluArgGluAsnSerSerThrAspAlaProProGlnProGluThrValThrAlaThrVal

ProAlaValGlnThrAsnThrAlaGluAlaLeuArgGluArgLysGluGluIleLysArg

GlnLysGlnAspGluGluGlyLeuHisLeuLeuThrLeuLeuLeuGlnCysAlaGluAla

ValSerAlaAspAsnLeuGluGluAlaAsnLysLeuLeuLeuGluIleSerGlnLeuSer

ThrProTyrGlyThrSerAlaGlnArgValAlaAlaTyrPheSerGluAlaMetSerAla

FIG. 5E-1

ArgLeuLeuAsnSerCysLeuGlyIleTyrAlaAlaLeuProSerArgTrpMetProGln

ThrHisSerLeuLysMetValSerAlaPheGlnValPheAsnGlyIleSerProLeuVal

LysPheSerHisPheThrAlaAsnGlnAlaIleGlnGluAlaPheGluLysGluAspSer

ValHisIleIleAspLeuAspIleMetGlnGlyLeuGlnTrpProGlyLeuPheHisIle

LeuAlaSerArgProGlyGlyProProHisValArgLeuThrGlyLeuGlyThrSerMet

GluAlaLeuGlnAlaThrGlyLysArgLeuSerAspPheThrAspLysLeuGlyLeuPro

PheGluPheCysProLeuAlaGluLysValGlyAsnLeuAspThrGluArgLeuAsnVal

ArgLysArgGluAlaValAlaValHisTrpLeuGlnHisSerLeuTyrAspValThrGly

SerAspAlaHisThrLeuTrpLeuLeuGlnArgLeuAlaProLysValValThrValVal

GluGlnAspLeuSerHisAlaGlySerPheLeuGlyArgPheValGluAlaIleHisTyr

TyrSerAlaLeuPheAspSerLeuGlyAlaSerTyrGlyGluGluSerGluGluArgHis

ValValGluGlnGlnLeuLeuSerLysGluIleArgAsnValLeuAlaValGlyGlyPro

SerArgSerGlyGluValLysPheGluSerTrpArgGluLysMetGlnGlnCysGlyPhe

LysGlyIleSerLeuAlaGlyAsnAlaAlaThrGlnAlaThrLeuLeuLeuGlyMetPhe

ProSerAspGlyTyrThrLeuValAspAspAsnGlyThrLeuLysLeuGlyTrpLysAsp

LeuSerLeuLeuThrAlaSerAlaTrpThrProArgSerSTOP

FIG. 5E-2

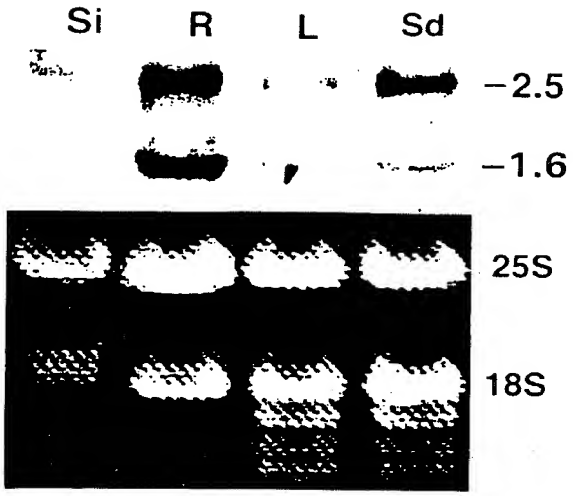


FIG.6A

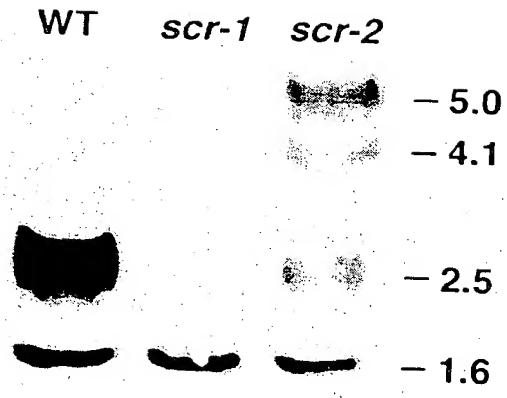


FIG.6B

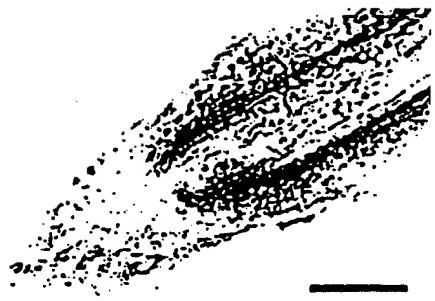


FIG.7A

FIG.7B

FIG.7C

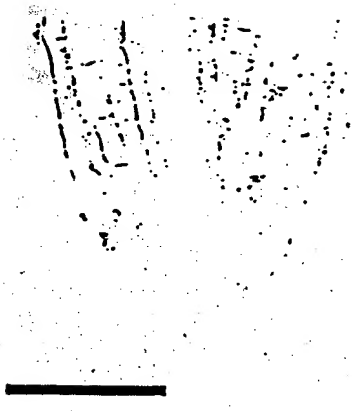


FIG.7D

FIG.7E

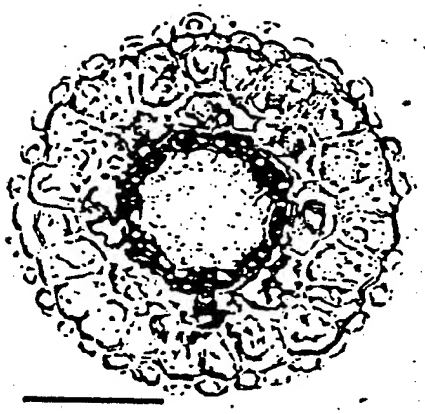


FIG.7F

FIG.7G

```
        10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
GGCACGAGCC CAACGGGTCC TGAGCTTCTT ACTTATATGC ATATCTTGTA    50
G T S P  T G P  E L L  T Y M H  I L Y

TGAAGCCTGC CCTTATTTCA AATTCGGTTA TGAATCTGCT AATGGAGCTA   100
 E A C  P Y F K  F G Y  E S A  N G A I

TAGCTGAAGC TGTGAAGAAC GAAAGTTTTG TGCACATTAT CGATTTCCAG   150
  A E A  V K N  E S F V  H I I  D F Q

ATTTCTCAAG GTGGTCAATG GGTGAGTTTG ATCCGTGCTC TTGGTGCTAG   200
I S Q G  G Q W  V S L  I R A L  G A R

ACCTGGTGGA CCTCCGAACG TTAGGATAAC GGGAATTGAT GATCCGAGAT   250
 P G G  P P N V  R I T  G I D  D P R S

CATCGTTTGC TCGTCAAGGA GGACTTGAGT TAGTTGGACA AAGACTTGGG   300
  S F A  R Q G  G L E L  V G Q  R L G

AAGCTAGCTG AAATGTGCGG TGTTCCGTTT GAGTTCCATG GAGCTGCTTT   350
K L A E  M C G  V P F  E F H G  A A L

ATGCTGCACG GAAGTCGAAA TCGAGAAGCT AGGAGTTAGA AATGGAGAAG   400
 C C T  E V E I  E K L  G V R  N G E A

CGCTCGCGGT TAACTTCCCG CTTGTTCTTC ACCACATGCC TGATGAGAGT   450
  L A V  N F P  L V L H  H M P  D E S

GTAACTGTGG AGAATCACAG AGATAGATTG TTGAGATTGG TCAAACACTT   500
V T V E  N H R  D R L  L R L V  K H L

GTCACCAAAC GTTGTGACTC TGGTTGAGCA AGAAGCGAAT ACAAACACTG   550
 S P N  V V T L  V E Q  E A N  T N T A

CGCCGTTTCT TCCCCGGTTT GTCGAGACAA TGAACCATTA CTTGGCAGIT   600
  P F L  P R F  V E T M  N H Y  L A V
```

FIG.8A

```
         10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
TTCGAATCAA TAGATGTGAA ACTCGCTAGA GATCACAAGG AAAGGATCAA  650
F  E  S  I  D  V  K  L  A  R  D  H  K  E  R  I  N

TGTTGAGCAG CATTGTTTGG CTAGAGAGGT TGTGAATCTT ATAGCTTGTG  700
 V  E  Q  H  C  L  A  R  E  V  V  N  L  I  A  C  E

AAGGTGTTGA AAGAGAAGAG AGGCACGAGC CACTAGGGAA ATGGAGGTCT  750
  G  V  E  R  E  E  R  H  E  P  L  G  K  W  R  S

CGGTTTCACA TGGCGGGATT TAAACCGTAT CCTTTGAGCT CGTATGTGAA  800
R  F  H  M  A  G  F  K  P  Y  P  L  S  S  Y  V  N

CGCAACAATC AAAGGATTGC TTGAGAGTTA TTCAGAGAAG TATACACTTG  850
 A  T  I  K  G  L  L  E  S  Y  S  E  K  Y  T  L  E

AAGAAAGAGA TGGAGCATTG TATTTAGGAT GGAAGAATCA ACCTCTTATC  900
  E  R  D  G  A  L  Y  L  G  W  K  N  Q  P  L  I

ACTTCTTGTG CTTGGAGGTA ACTAATAAAA ACCTTGTTCG GTTTCAGAAG  950
T  S  C  A  W  R  X

AGATTAGAAA CTTCTTTTAA AGTTTGCAGA ATCTGTTTGT AAAAGTAAAA 1000

CTCATGCATG ATCCGNAGGA ACAAGTTGTC AAATGTTGTA GTAGTAAGTG 1050

ATATGTTGAT GACCCAAAAA AAAAAAAAAA AAAAA                  1085
```

FIG.8B

```
          10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
GCTATGGAAG GAGAGAAGAT GGTTCATGTG ATTGATCTCG ATGCTTCTGA   50
A M E G  E K M  V H V  I D L D  A S E

GCCAGCTCAA TGGCTTGCTT TGCTTCAAGC TTTTAACTCT AGGCCTGAAG  100
 P A Q  W L A L  L Q A  F N S  R P E G

GTCCACCTCA TTTGAGAATC ACTGGTGTTC ATCACCAGAA GGAAGTGCTT  150
  P P H  L R I  T G V H  H Q K  E V L

GAACAAATGG CTCATAGACT CATTGAGGAA GCAGAGAAAC TCGATATCCC  200
E Q M A  H R L  I E E  A E K L  D I P

GTTTCAGTTT AATCCCGTTG TGAGTAGGTT AGACTGTTTA AATGTAGAAC  250
 F Q F  N P V V  S R L  D C L  N V E Q

AGTTGCGGGT TAAAACAGGA GAGGCCTTAG CCGTTAGCTC GGTTCTTCAA  300
  L R V  K T G  E A L A  V S S  V L Q

TTGCATACCT TCTTGGCCTC TGATGATGAT CTCATGAGAA AGAACTGCGC  350
L H T F  L A S  D D D  L M R K  N C A

TTTACGGTTT CAGAACAACC CTAGTGGAGT TGACTTGCAG AGAGTTCTAA  400
 L R F  Q N N P  S G V  D L Q  R V L M

TGATGAGCCA TGGCTCTGCA GCTGAGGCAC GTGAGAATGA TATGAGTAAC  450
  M S H  G S A  A E A R  E N D  M S N

AACAATGGGT ATAGCCCTAG CGGTGAGTCG GCCTCATCTT TGCCTTTACC  500
N N G Y  S P S  G D S  A S S L  P L P

AAGTTCAGGA AGGACTGATA GCTTCCTCAA TGCTATTTGG GGTTTGTCTC  550
 S S G  R T D S  F L N  A I W  G L S P

CAAAGGTCAT GGTGGTCACT GAGCAAGACT CAGACCACAA CGGCTCCACA  600
  K V M  V V T  E Q D S  D H N  G S T
```

FIG.9A

```
          10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
CTAATGGAGA GGCTATTAGA ATCACTTTAC ACCTACGCAG CATTGTTTGA   650
L M E R  L L E  S L Y  T Y A A  L F D

TTGCTTGGAA ACAAAAGTTC CAAGAACGTC TCAAGATAGG ATCAAAGTGG   700
 C L E  T K V P  R T S  Q D R  I K V E

AGAAGATGCT CTTCGGGGAG GAGATCAAGA ACATCATATC CTGCGAGGGA   750
  K M L  F G E  E I K N  I I S  C E G

TTTGAGAGAA GAGAAAGACA CGAGAAGCTT GAGAAATGGA GCCAGAGGAT   800
F E R R  E R H  E K L  E K W S  Q R I

DGATTTGGCT GGTTTTGGGA ATGTTCCTCT TAGCTATTAT GCGATGTTGC   850
 D L A  G F G  N V P  L S Y  Y A M  L Q

AGGCTAGGAG ATTGCTTCAA GGGTGCGGTT TTGATGGGTA TAGAATCAAG   900
  A R R  L L Q  G C G  F D G  Y R I  K

GAAGAGAGCG GGTGCGCAGT AATTTGCTGG CAAGATCGAC CTCTATACTC   950
E E S G  C A V  I C W  Q D R  P L Y  S

GGTATCAGCT TGGAGATGCA GGAAGTGAAT GATATATTAC AGTTTGTCTT  1000
 V S A  W R C  R K X

CTATTTTGGT TATGAGCAGA GTCCCTTTCT TTTTTGTATA CATGGGGACA  1050

CAATCTTAGT TGTTTTGTGA TGGTGACTTT CTGTCTCTTT ATGCTATTTT  1100

GGCTTAAATG CTTCTACTGC CTCTGCATGT AAAGCCTTTG TGTGTTGGTT  1150

CAATTTGGTC TGGTGTGGGT GTAATACCAA ACCAAATCCA ATTTGAGCTG  1200

AAGATAACTA ATTTGATGAT CGGCTCGTGC C                      1231
```

FIG.9B


```
CTTTGTCAAT GGTAAATGAG CTGAGGCAGA TAGTTTCTAT CCAAGGAGAC      50
CCTTCTCAGA GAATCGCAGC TTACATGGTG GAAGGTCTAG CTGCAAGAAT     100
GGCCGCTTCA GGAAAATTCA TCTACAGAGC ATTGAAATGC AAAGAGCCTC     150
CTTCGGATGA GAGGCTTGCA GCTATGCAAG TCCTGTTTGA AGTCTGCCCT     200
TGTTTCAAGT TCGGGTTTTT AGCAGCTAAT GGTGCGATAC TTGAAGCAAT     250
CAAAGGTGAA GAAGAAGTTC ACATAATCGA TTTCGATATA AACCAAGGGA     300
ACCAATACAT GACACTGATA CGAAGCATTG CTGAGTTGCC TGGTAAACGA     350
CCTCGCCTGA GGTTAACAGG AATTGATGAC CCTGAATCAG TCCAACGCTC     400
CATTGGAGGG CTAAGAATCA TCAATCTAAG ACTCGAGCAA CTCGCAGAGG     450
ATAATGGAGT ATCCTTCAAA TTCAAAGCAA TGCCTTCAAA GACTTCGATT     500
GTCTCTCCAT CAACACTCGG TTGCAAACCA GGAGAAACCT TAATCAGTGA     550
ACTTTGCATT CCAACTTCAC CACATGCCTG ACGAGAGTGT CACAACAGTA     600
AACCAGCGGG ACGAGCTACT TCACATGGTC AAAAGCTTAA ACCCGCTTGT     650
CACGGTCGTT GAACAAGACG TGAACACAAA CACTTCACCG TTCTTTCCCA     700
GATTCATAGA GGCTTACGAA TACTACTCAG CAGTTTTCGA GTCTCTAGAC     750
ATGACACTTC CAAGAGAAAG CCAAGAGAGG ATGAATGTAG AAAGACAGTG     800
TCTCGCTAGA GACATAGTCA ACATTGTTGC TTGCGAAGGA GAAGAACGGA     850
TAGAGAGATA CGAGGCTGCG GGAAAATGGA GAGCAAGGAT GATGATGGCT     900
GGATTCAATC CAAAACCAAT GAGTGCTAAA GTAACCAACA ATATACAAAA     950
CCTGATAAAG CAACAATATT GCAATAAGTA CAAGCTTAAA GAAGAAATGG    1000
GTGAGCTCCA TTTTTGCTGG GAGGAGAAAA GCTTAATCGT TGCTTCAGCT    1050
TGGAGGTAAG ATAAGTGACA AGAGCATATA GTCTTTATGT TTCATAAAAC    1100
ATAATTATGT TTTTACTGTA ATCTTGGGTT ATTGTGTAAC TGGTTAAATC    1150
ATCTCCATGT ATTATTACCA GAGGTTAGGG GTGATCACAG GTACTAAAAG    1200
CTAATCTAAC ACTTATGGAA GAATTTTTCT TTCTTTTTTT TCCCTATTAT    1250
ATAAAAATAA TTAGAGTTTT GGTTCTAAAC CTATTTGCTA AGTGTGAATG    1300
AGTCTTTACA TGTTCATATT TCAGTTCAAA TGGTTAAATT TGTTAAGGTT    1350
CTCACTTAAA AAAAAA
```


FIG. 10

Zm-scl1

```
        10         20         30         40         50
CCAGGAGGCGTTCGAGCGGGAGGAGCGTGTGCACATCATCGACCTCGACA
 Q  E  A  F  E  R  E  E  R  V  H  I  I  D  L  D  I

        60         70         80         90        100
TCATGCAGGGGCTGCAGTGGCCGGGCCTCTTCCACATCCTTGCCTCCCGC
 M  Q  G  L  Q  W  P  G  L  F  H  I  L  A  S  R
```

FIG.11A

```
        10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
CACGCGTCCG TCAAAGGATA CAACCATGTA CACATAATTG ACTTTTCCCT   50
H A S V  K G Y  N H V  H I I D  F S L

GATGCAAGGT CTCCAGTGGC CGGCACTCAT GGATGTCTTC TCCGCCCGTG  100
 M Q G  L Q W P  A L M  D V F  S A R E

AGGGTGGGCC ACCAAAGCTC CGAATCACAG GCATTGGCCC GAACCCAATA  150
  G G P  P K L  R I T G  I G P  N P I

GGTGGCCGTG ACGAGCTCCA TGAAGTGGGA ATTCGCCTCG CCAAGTATGC  200
G G R D  E L H  E V G  I R L A  K Y A

ACACTCGGTG GGTATCGACT TCACTTTCCA GGGAGTCTGT GTCGATCAAC  250
 H S V  G I D F  T F Q  G V C  V D Q L

TTGATAGGTT GTGCGACTGG ATGCTTCTCA AACCAATCAA AGGAGAGGCA  300
  D R L  C D W  M L L K  P I K  G E A

GTTGCCATAA ACTCCATCCT ACAACTCCAT CGCCTCCTCG TTGACCCAGA  350
V A I N  S I L  Q L H  R L L V  D P D

TGCAAACCCA GTGGTGCCCG CACCAATAGA TATCCTCCTC AAATTGGTCA  400
 A N P  V V P A  P I D  I L L  K L V I

TCAAGATAAA CCCCATGATC TTCACGGTGG TTGAGCATGA GGCAGATCAC  450
  K I N  P M I  F T V V  E H E  A D H

AACAGACCAC CACTACTAGA GAGGTTCACT AATGCCCTCT TCCACTATGC  500
N R P P  L L E  R F T  N A L F  H Y A

GACCATGTTT GACTCTTTGG AGGCCATGCA TCGTTGTACC AGTGGTAGAG  550
 T M F  D S L E  A M H  R C T  S G R D

ACATCACCGA CTCACTCACA GAGGTGTACC TTCGAGGTGA GATTTTTGAC  600
  I T D  S L T  E V Y L  R G E  I F D
```

FIG.11B1

```
          10         20         30         40         50
1234567890 1234567890 1234567890 1234567890 1234567890
ATTGTCTGCG GCGAGGGCAG TGCACGCACC GAACGTCATG AGTTGTTTGG   650
I V C G  E G S  A R T  E R H E  L F G

TCACTGGAGG GAGAGGCTCA CCTATGCTGG GCTAACTCAA GTGTGGTTCG   700
 H W R  E R L T  Y A G  L T Q  V W F D

ACCCCGATGA GGTTGACACG CTAAAAGACC AGTTGATCCA TGTGACATCC   750
  P D E  V D T  L K D Q  L I H  V T S

TTATCTGGCT CTGGGTTCAA CATCCTAGTG TGTGATGGCA GCCTTGCACT   800
L S G S  G F N  I L V  C D G S  L A L

AGCGTGGCAT AATCGCCCGT TATATGTGGC AACAGCTTGG TGTGTGACAG   850
 A W H  N R P L  Y V A  T A W  C V T G

GAGGAAATGC TGCCAGTTCC ATGGTTGGCA ACATCTGTAA GGGTACAAAT   900
  G N A  A S S  M V G N  I C K  G T N

GATAGTAGAA GAAAGGAAAA CCGTAATGGA CCCATGGAGT AGCAGGAAGA   950
D S R R  K E N  R N G  P M E  X

ATAACCATGT CATGAGCAAA TCGATCAAGT AATAAAATGC ACTGATGACA  1000

TGCATGGTGA TCTAAAGTTT TTTTGCGTGA ATGTGCAATG ACGAATTGTT  1050

CAATTTGAAT AACCTAATCA TGAGACTCAA AAAAAAAAAA AAA          1093
```

FIG.11B2

```
CCCAACTTGG GAAGCCCTTC CTCCGCTCCG CCTCCTACCT CAAGGAGGCC        50
CTCCTCCTCG CACTCGCCGA CAGCCACCAT GGCTCCTCCG GCGTCACCTC       100
GCCGCTCGAC GTTGCCCTCA AGCTTGCAGC ATACAAGTCT TTCTCTGACC       150
TGTCACCTGT GCTCCAGTTC ACTAACTTTA CCGCAACAAG GCGCTTCTTG       200
ATGAGATTGG TGGCATGGCA ACTTCCTGCA TCCATGTCAT TGACTTTGAT       250
CTCGGTGTTG GTGGTCAGTG GGCTTCCTTC TTGCAGGAGC TTGCCCACCG       300
CCGGGGAGCT GGAGGTATGG CCTTGCCGTT GTTGAAGCTC ACGGCTTTCA       350
TGTCGACTGC TTCTCACCAT CCACTGGAGC TGCACCTTAC CCAGGATAAC       400
CTCTCTCAGT TTGCCGCAGA GCTCAGAATT CCTTTCGAAT TCAATGCCGT       450
CAGTCTTGAT GCATTCAATC CTGCGGAATC TATTTCTTCC TCTGGTGATG       500
AAGTTGTTGC TGTTAGCCTC CCTGTTGGCT GCTCTGCTCG TGCACCACCG       550
CTGCCAGCGA TTCTTCGGTT GGTGAAACAG CTTTGTCCTA AGGTTGTCGT       600
GGCTATTGAT C
```

FIG. 12A

```
TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TACAGAGCAA CAGCAGTATA      50
ATATTAATTC TGTACCACAC AACCATTTGA TAGGTTAAAT TACCCTCTAG     100
TCTCTACTCA TAAGCAGTGT TTCCAATGAG ATGATCATGG CTAATTGAGC     150
AGAGCATGGC AACAACCTAA AGCAACATCA TTAGCTATAG AGACTGACAC     200
CAATATTCCT AAATCCACTA GGCTAGCTAA TAAGCTGCAA CGAAAAGCAA     250
TATGAAGAGT TCAACAGCTC AAGACAACAA TTTCATTTGC AACATTTAAT     300
TGCAAGAATA AATGGACATT ACTGGAGTGG TCGATGCTTG CAAACGGTGG     350
TGGAACCTTG GTGGAGTGAA GCTTATGGCT GATCAGCACC GCCAAGATGA     400
TATGGATACA AGCTCCCCAC GCTGCCAGTA GAGCGTAAGA GCAGCTCCGC     450
GTTTCTCCAC ATGGAATCCT CGGACCTGCA CCCGCTTCAG GAGGCAGTCT     500
GC
```

FIG. 12B

```
SCR     MAESGDFNGGQPPPHSPLRTTSSGSSSSNNRGPPPPPPPPLVMVRKR----LASEMSS
TF1     MKRD---HHQFQGRLSNHGTSSSSSSISKDK--MMMVKKEEDGGGNMDDELLAV----
TF4     MKRDHHHHHQ----------------------DKKTMMM--NEEDDGNGM-DELLAV----

                |-------------- MOTIF  I --------------|
SCR     NPDYNNSSRPPRRVSHLLDSNYNTVTPQQPPSLTAAATVSSQPNPPLSVCGFSG
TF1     -LGYKVRSSEMAEVALKLEQLETMMSNAQEDGLSHLATDAAHYNPSELYS----
TF4     -LGYKVRSSEMADVAQKLEQLEVMMSNVQEDDLSQLATETVHYNPAELYT----

SCR     LPVFPSDRGGRNVMMSVQPMDQDSSSSSASPTVWVDAIIRDLIHS----STSVSIPQL
TF1     ------------------------------------WLDNMLSELNPPPLPASSNGLDPVL
TF4     ------------------------------------WLDSMLTDLNPP----SSN-AEYDL

SCR     IQNVRDIIFPCNPNLGALLEYRLRSLMLLDPSSSSDPSPQTFEPLYQISNNPSP
TF1     PSPEICGFPXSDYDLKVIPXNAIYQFPAIDSSSSSNN--Q--------------
TF4     -----KAI-P---------GDILNQF-AIDSASSSN---Q--------------
```

FIG. 13A

```
                                                                    |-----
SCR       PQQQQQHQQQQQQQHKPPPPPIQQQERENSSTDAPPQPETVTATVPAVQTNTAEA
TF1       ----------NKRLKSCSSPDSMVTSTSTGTQIGGVIGTTVTTTTTTTTAAAES
TF4       ------------------------GGGGDTYTTNKRLKCSNGVVETTTATAES

          -------- MOTIF II (DIMERIZATION?) ----------------
SCR       LRERKEEIKRQKQDEEGLHLLTLLLQCAEAVSADNLEEANKLLLEISQLSTPYG
1110                                                LSMVNELRQIVSIQG
TF1       ----TRSVILVDSQENGVRLVHALMACAEAIQQNNLTLAEALVKQIGCLAVSQA
TF4       ----TRHVVLVDSQENGVRLVHALLACAEAVQKENLTVAEALVKQIGFLAVSQI
3898                                                        QLGKPFL

          ----------------|                                 |-----
SCR       TSAQRVAAYFSEAMSARLLNSCLGIYAALPSRWMPQTHSLKMVSAFQVFNGISP
4818                                              GTSPT-GPELLTYMHILYEACP
1110      DPSQRIAAYMVEGLAARMAASGKFIYRAL-KCKEPPS--DERLAAMQVLFEVCP
TF1       GAMRKVATYFAEALARR-------IY-RL-SPPQNQIDHCLSDTLQMHFYETCP
TF4       GAMRQVATYFAEALARR-------IY-RL-SPSQSPIDHSLSDTLQMHFYETCP
3989      ----RSASYLKEALLLALADSHHGSSGVT-SPLDVA----LKLAAYKSFSDLSP
```

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FIG.13B

```
                    ------------------- MOTIF III  (VHIID)  -----------
SCR       LVKFSHFTANQAIQEAFEK--EDSVHIIDLDIMQGLQWPGLFHILASRPGGPP----HVR
4818      YFKFGYESANGAIAEAVKN--ESFVHIIDFQISQGGQWVSLIRALGARPGGPP----NVR
1110      CFKFGFLAANGAILEAIKG--EEEVHIIDFDINQGNQYMTLIRSIAELPGKRP----RLR
3935                        AMEG--EKMVHVIDLDASEPAQWLALLQAFNSRPEGPP----HLR
TF1       YLKFAHFTANQAILEAFEG--KKRVHVIDFSMNQGLQWPALMQALALREGGPP----TFR
TF4       YLKFAHFTANQAILEAFQG--KKRVHVIDFSMSQGLQWPALMQALALRPGGPP----VFR
3989      VLQFTNFTANKALLDEIGGMATSCIHVIDFNLGVGGQWASFLQELAHRRGAGGMALPLLK
18310                     HASVKG--YNHVHIIDFSLMQGLQWPALMDVFSAREGGPP----KLR
Zm-Scl1                   QEAFER--EERVHIIDLDIMQGLQWPGLFHILASR
Zm-Scl2                     FAG--CRRVHVVDFGIKQGMQWPALLXDLAL
Human                    GRNGRTL--WLGEGHIDLWPLQGLLSQGLQRALCARPLGAP---HVF-
```

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FIG. 13C

```
                                                        |-------------- MOTIF  V  -
          --||-------------- MOTIF  IV  (DIMERIZATION )  ------------------|
SCR       LTG  LGTSMEA       LQATGKR  LSDFTDK  LGLPFEFCPLAEKVGNDLTERLNV
4818      ITGIDDPRSSFARQGG   LELVGQR  LGKLAEM  CGVPFEFHGAALCCTEVEIEKLGV
1110      LTGIDDPESVQRSIGG   LRIINLR  LEQLAED  NGVSFKFKAMPSKTSIVSPSTLGC
3935      ITG  VHHQKEV       LEQMAHR  LIEEAEK  LDIPFQFNPVVSRLDCLNVEQLRV
TF1       LTGIGPPAPDNSDH     LHEVGCK  LAQLAEA  IHVEFEYRGF  VANSLAD  LDASMLELRP
TF4       LTGIGPPAPDNFDY     LHEVGCK  LAHLAEA  IHVEFEYRGF  VANTLAD  LDASMLELRP
3989      LTAFMSTASHHPLE     LHLTQDN  LSQFAAE  LRIPFEFNAVSLDAFNPAESISSSGDE
18310     ITGIGPNPIGGRDE     LHEVGIR  LAKYAHS  VGIDFTFQGVCVDQLDRLCDWMLLKPI
Human     LPGLHTLS...        LGLQXRH  LLVHMMA  LSYSYGRXP...
```

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```
          --------------|
SCR       RKREAAVHWLQHSLYDVTGSDAHTLWLL---QRLAPK------------------
4818      RNGEALAVNFPLVLHHMPDESVTVENHR---DRLLRL------------------
1110      KPGETL VNFAFQLHHMPDESVTTVNQR---DELLHM------------------
3935      KTGEALAVSSVLQLHTFLASDDDLMRKNC-ALRFQNNPSGVDLQRVLMMSHGS
TF1       SDTEAVAVNSVFELHKLLGRXGGIEKVLG----------------------
TF4       SEIESVAVNSVFELHKLLGRPGAIDKVLG----------------------
18310     K-GEAVAINSILQLHRLLVDPDANPVVPAPIDILLK---
3989      VVAVSLPVGCSARAPPLPAILRLVKQLCPKVVVAID
```

FIG. 13D

```
                                                                    |----
SCR      ----------------------------------------------------------VVTV-
4818     ---------------------------------------------VKHLSPN-VVTL-
1110     ---------------------------------------------VKSLNPK-LVTV-
3935     AAEARENDMSNNNGYSPSGDSASSLPLPSSGRTDSFLNAIWGLSPKVMVVT-
TF1      ---------------------------------------------VVKQD*TGDFHXW
TF4      ---------------------------------------------VVNQIKPEIFTV-
18310    ---------------------------------------------LVIKINPMIFTV-


         ----------------  MOTIF  VI  ----------------------
SCR      VEQDLSHAGS--FLG-RFVEAIHYYSALFDSLGASYGEESE---ERHVVEQQ
4818     VEQEANTNTAP-FLP-RFVETMNHYLAVFESIDVKLARDHK---ERINVEQH
1110     VEQDVNTNTSP-FFP-RFIEAYEYYSAVFESLDMTLPRESQ---ERMNVERQ
3935     -EQDSDHNGS--TLMERLLESLYTYAALFDCLETKVPRTSQ---DRIKVEKM
TF1      XRQEPNHNG-PGFLD-GXTESLHYYSTXFDSLEG--XPNSQ---DKLMSEXY
TF4      VEQESNHNS-PIFLD-RFTESLHYYSTLFDSLEG--VPSGQ---DKVMSEVY
18310    VEHEADHNR-PPLLE-RFTNALFHYATMFDSLEAMHTCTSGRDITDSLTEVY
```

FIG. 13E

```
          ----------------------------------------
SCR       LLSKEIRNVLAVGGPSRSGEVKFE-SWREKMQQCGFKGIS-
4818      CLAREVVNLIACEGVEREERHEPLGKWRSRFHMAGFKPYP-
1110      CLARDIVNIVACEGEERIERYEAAGKWRARMMMAGFNPKP-
3935      LFGEEIKNIISCEGFERRERHEKLEKWSQRIDLAGFGNVP-
TF1       -LGXQICNLVACEGPDRVERHETLSQWGNRFGSSGLAPAH-
TF4       -LGKQICNVVACDGPDRVERHETLSQWRNRFGSAGFAAAH-
18310     -LRGEIFDIVCGEGSARTERHELFGHWRERLTYAGLTQVWF

          ----------------------------------------|
SCR       LAGNAATQATLLLGMFPS-DGYTLVDDN-GTLKLGWKDLSLLTASAWTPRS*
4818      LSSYVVNATIKGLLES-YS-EKYTL-EERDGALYLGWKNQPLITSCAWR*
1110      MSAKVTNNIQNLIKQQYC-NKYKLKEEM-GELHFCWEEKSLIVASAWR*
3935      LSYYAMLQARRLLQGCGF-DGYRIKEES-GCAVICWQDRPLYSVSAWRCRK*
TF1       LGSNAFKQASMLLSVFNSGQGYRV-EESNGCLMLGWHTRPLITTSAWKLSTAAH*
TF4       IGSNAFKQASMLLALFNGGEGYRV-EESDGCLMLGWHTRPLIATSAWKLSTN*
3989         ADCLL-KRVQVRGFHV-EKRGAALTLYWQRGELVSISSWRC*
18310     DPDEVDTLKDQLIHVTSLSGSGFNILVCDGSLALAWHNRPLYVATAWCVTGGNAA

18310     SSMVGNICKGTNDSRRKENRNGPME*
```

FIG. 13F

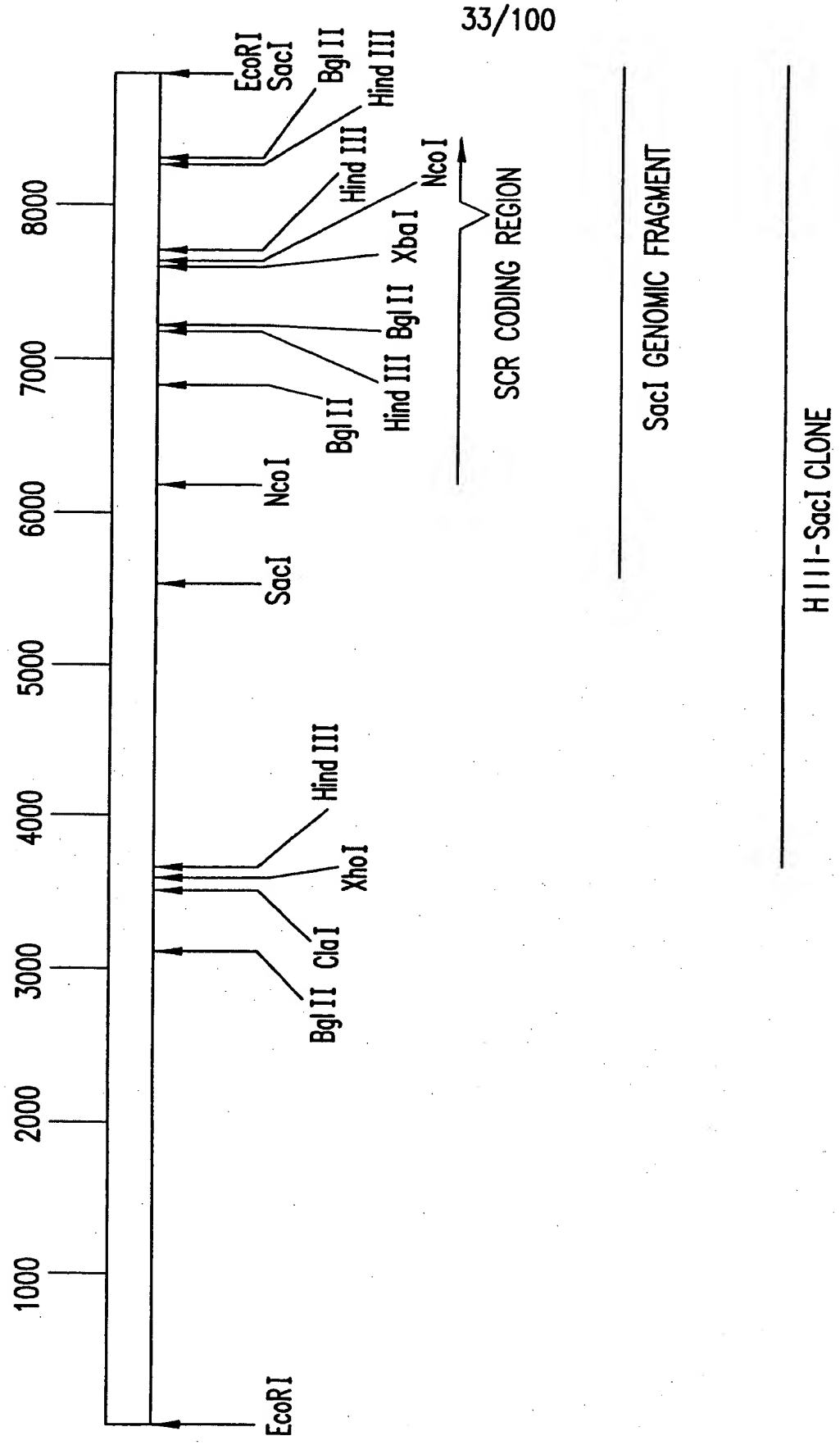


FIG. 14

Old Name						New Name
Scr	.....	.....	.....	.....	.....	*SCR*
3989	.....	.....	.....	.....	.....	*SRPo3*
12398	.....	.....	.....	.....	.....	*SRPa6*
4871	.....	.....	.....	.....	.....	*SRPa5*
11846	.....	.....	.....	.....	.....	*SRPo4*
2504	.....	.....	.....	.....	.....	*SRPo2*
3935	.....	.....	.....	.....	.....	*SRPa3*
11261	.....	.....	.....	.....	.....	*SRPa10*
713	.....	.....	.....	.....	.....	*SRPo1*
10964	.....	.....	.....	.....	.....	*SRPa9*
23196	LL	KVLLCHLVAE	STKRRIKIRP	LLDINDSGFL	GFWSWIHMGS	*SRPa12*
Tf1	.....	.....	.....	.....	.....	*SRPa8*
Tf4	.....	.....	.....	.....	.....	*SRPa2*
18310	.....	.....	.....	.....	.....	*SRPm1*
18652	.....	.....	.....	.....	.....	*SRPa11*
4818	.....	.....	.....	.....	.....	*SRPa4*
21729	.....	.....	.....	.....	.....	*SRPa7*
1110	.....	.....	.....	.....	.....	*SRPa1*
174	.....	.....	.....	.....	.....	*SRPb1*
33/08	.....	.....	.....	.....	.....	*SRPa13*
	-150				-101	

FIG. 15A

```
  Scr  .......... .......... .......... .......... ..........
 3989  .......... .......... .......... .......... ..........
12398  .......... .......... .......... .......... ..........
 4871  .......... .......... .......... .......... ..........
11846  .......... .......... .......... .......... ..........
 2504  .......... .......... .......... .......... ..........
 3935  .......... .......... .......... .......... ..........
11261  .......... .......... .......... .......... ..........
  713  .......... .......... .......... .......... ..........
10964  .......... .......... .......... .......... ..........
23196  YPDGFPGSMD ELDFNKDFDL PPSSNQTLGL ANGFYLDDLD FSSLDPPEAY
  Tf1  .......... .......... .......... .......... ..........
  Tf4  .......... .......... .......... .......... ..........
18310  .......... .......... .......... .......... ..........
18652  .......... .......... .......... .......... ..........
 4818  .......... .......... .......... .......... ..........
21729  .......... .......... .......... .......... ..........
 1110  .......... .......... .......... .......... ..........
  174  .......... .......... .......... .......... ..........
33/08  .......... .......... .......... .......... ..........
       -100                                          -51
```

FIG. 15B

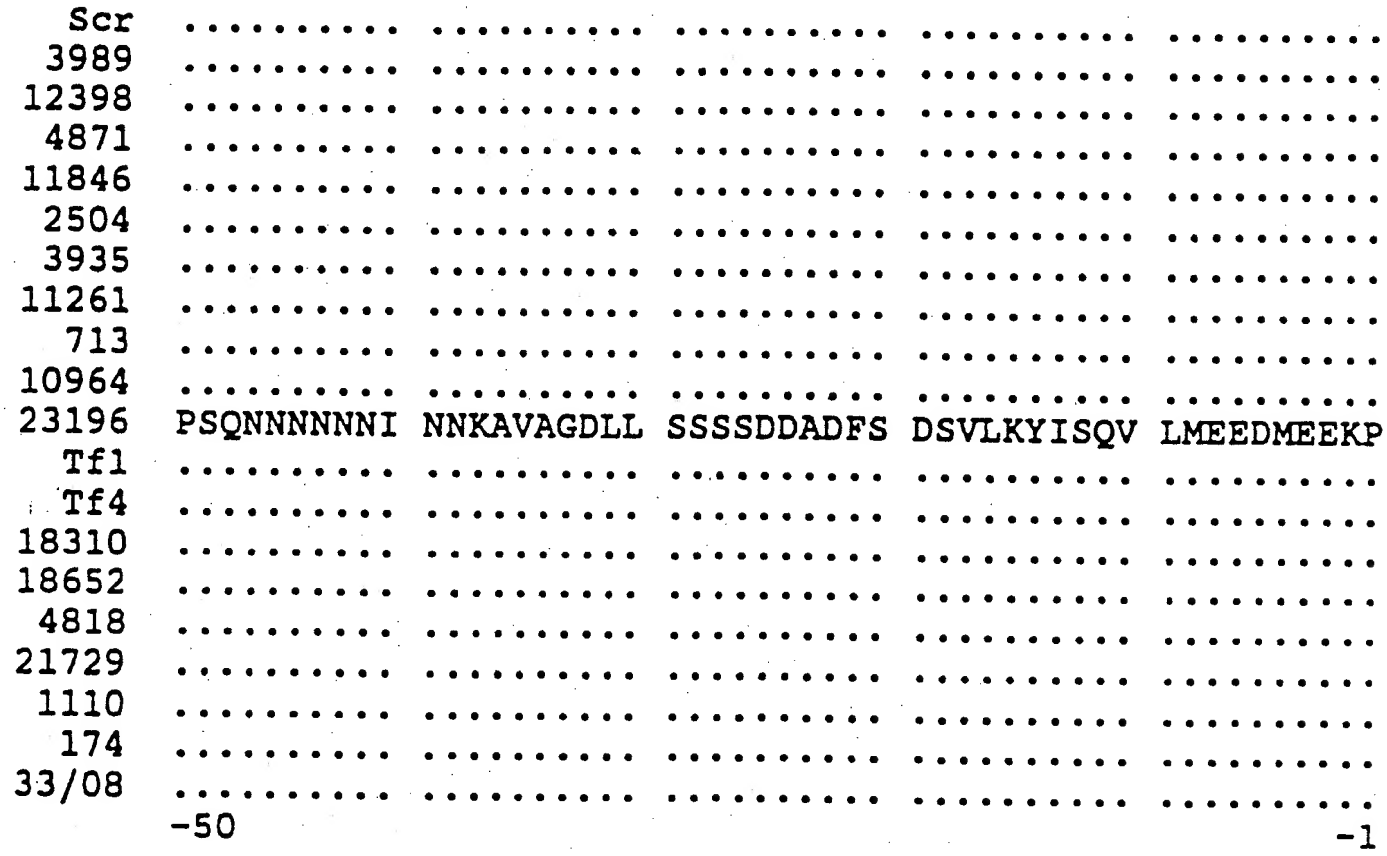


FIG. 15C

```
  Scr  MAESGDFNGG QPPPHSPLRT TSSGSSSSNN RGPPPPPPPP LVMVRKRLAS
 3989  .......... .......... .......... .......... ..........
12398  .......... .......... .......... .......... ..........
 4871  .......... .......... .......... .......... ..........
11846  .......... .......... .......... .......... ..........
 2504  .......... .......... .......... .......... ..........
 3935  .......... .......... .......... .......... ..........
11261  .......... .......... .......... .......... ..........
  713  .......... .......... .......... .......... ..........
10964  .......... .......... .......... .......... ..........
23196  CMFHDALALQ AAEKSLYEAL GEKDPSSSSA SSVDHPERLA SHSPDGSCSG
  Tf1  .......... .......... .......... .......... ..........
  Tf4  .......... .......... .......... .......... ..........
18310  .......... .......... .......... .......... ..........
18652  .......... .......... .......... .......... ..........
 4818  .......... .......... .......... .......... ..........
21729  .......... .......... .......... .......... ..........
 1110  .......... .......... .......... .......... ..........
  174  .......... .......... .......... .......... ..........
33/08  .......... .......... .....TSDSA SSFNIPTSAQ NHYATGSFST
       1                                                    50
```

FIG. 15D

```
                |<--------Motif I ---------------------------->|
  Scr   EMSSNPDYNN SSRPPRRVSH LLDSNYNTVT PQQPPSLTAA ATVSSQPNPP
 3989   .......... .......... .......... .......... ..........
12398   .......... .......... .......... .......... ..........
 4871   .......... .......... .......... .......... ..........
11846   .......... .......... .......... .......... ..........
 2504   .......... .......... .......... .......... ..........
 3935   .......... .......... .......... .......... ..........
11261   .......... .......... .......... .......... ..........
  713   .......... .......... .......... .......... ..........
10964   .......... .......... .......... .......... ..........
23196   GAFSDYASTT TTTSSDSHWS VDGLENRPSW LHTPMPSNFV FQSTSRSNSV
  Tf1   .......... .MKRDHHQFQ GRLSNHGTSS SSSSISKDKM MMVKKEEDGG
  Tf4   .......... .MKRDHHHHH .......... ......QDKK TMMMNEEDDG
18310   .......... .......... .......... .......... ..........
18652   .......... .......... .......... .......... ..........
 4818   .......... .......... .......... .......... ..........
21729   .......... .......... .......... .......... ..........
 1110   .......... .......... .......... .......... ..........
  174   .......... .......... .......... .......... ..........
33/08   NSRTTNVATA TTNSATAHWV ATDAEHTDTI IAQP
        51                                                  100
```

FIG. 15E

```
  Scr  LSVCGFSGLP VFPSDRGGRN VMMSVQPMDQ DSSSSSASPT VWVDAIIRDL
 3989  .......... .......... .......... .......... ..........
12398  .......... .......... .......... .......... ..........
 4871  .......... .......... .......... .......... ..........
11846  .......... .......... .......... .......... ..........
 2504  .......... .......... .......... .......... ..........
 3935  .......... .......... .......... .......... ..........
11261  .......... .......... .......... .......... ..........
  713  .......... .......... .......... .......... ..........
10964  .......... .......... .......... .......... ..........
23196  TGGGGGGNSA VYGSGFGDDL VSNMFKDDEL AMQFKKGVEE ASKFLPKSSQ
  Tf1  GNMDDELLAV LGYKVRSSEM AEVALKLEQL ETMMSNAQED GLSHLATDAA
  Tf4  NGM.DELLAV LGYKVRSSEM ADVAQKLEQL EVMMSNVQED DLSQLATETV
18310  .......... .......... .......... .......... ..........
18652  .......... .......... .......... .......... ..........
 4818  .......... .......... .......... .......... ..........
21729  .......... .......... .......... .......... .........D
 1110  .......... .......... .......... .......... ..........
  174  .......... .......... .......... .......... ..........
       101                                                  150
```

FIG. 15F

Scr	IHSSTSVSIP	QLIQNVRDII	FPCNPNLGAL	LEYRLRSLML	LDPSSSSDPS
3989	....	....	....	....	....
12398	....	....	....	....	....
4871	....	....	....	....	....
11846	....	....	....	....	....
2504	....	....	....	....	....
3935	....	....	....	....	....
11261	....	....	....	....	....
713	....	....	....	....	....
10964	....	....	....	....	....
23196	LFIDVDSYIP	MNSGSKENGS	EVFVKTEKKD	ETEHHHHHSY	APPPNRLTGK
Tf1	HYNPSELYSW	LDNMLSELNP	PPLPASSNGL	DPVLPSPEIC	GFPXSDYDLK
Tf4	HYNPAELYTW	LDSMLTDLNP	P....SSNA.	....	.....EYDLK
18310	....	....	....	....	....
18652	....	....	....	....	....
4818	....	....	....	....	....
21729	LTSVNDMSLF	GGSGSSQRYG	LPVPRSQTQQ	QQSDYGLFGG	IRMGIGSGIN
1110	....	....	....	....	....
174	....	....	....	....	....
	151				200

FIG. 15G

Scr	PQTFEPLYQI	SNNPSPPQQQ	QQHQQQQQQH	KPPPPPIQQQ	ERENSSTDAP
3989	....	....	....	....	....
12398	....	....	....	....	....
4871	....	....	....	....	....
11846	....	....	....	....	....
2504	....	....	....	....	....
3935	....	....	....	....	....
11261	....	....	....	....	....
713	....	....	....	....	....
10964	....	....	....	....	....
23196	KSHWRDEDED	VEERSNKQSA	VYVEESELSE	MFDNMFLCGP	GKPVCILNQN
Tf1	VIPXNAIYQF	PAIDSSSSSN	NQ.....	NKRLKSCSSP	DSMVTSTSTG
Tf4	AIPGDAILNQ	FAIDSASSSN	QGGGGDTYTT	NKRLKCS...	....
18310	....	....	....	....	....
18652	....	....	....	....	....
4818	....	....	....	....	....
21729	NYPTLTGVPC	IEPVQNRVHE	SENMLNSLRE	LEKQLLDDDD	ESGGDDDVSV
1110	....	....	....	....	....
174	....	....	....	....	....
	201				250

FIG. 15H

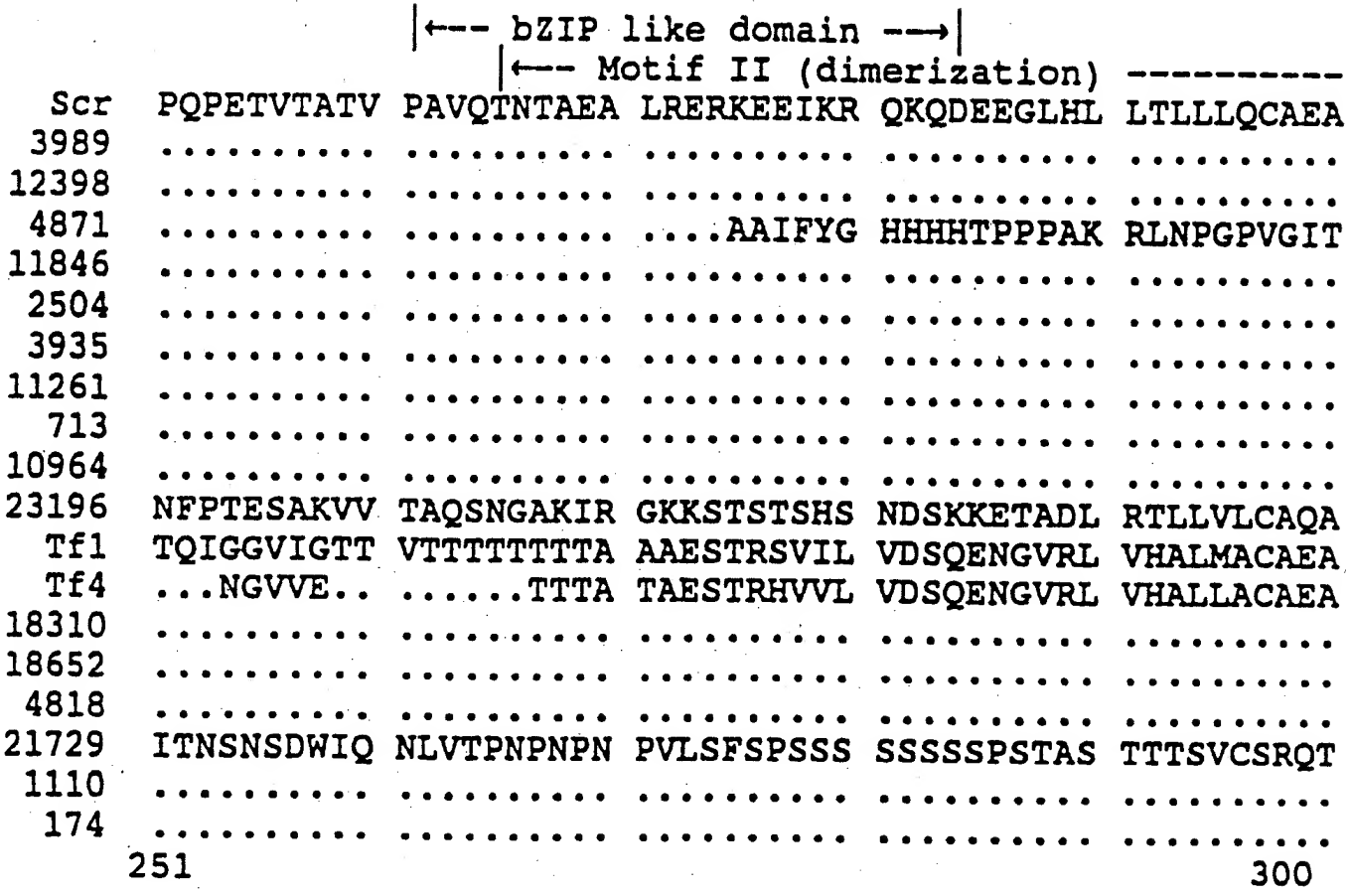


FIG. 151

```
      ------ Motif II (dimerization) ------------>|
 Scr  VSADNLEEAN KLLLEISQLS TPYGTSAQRV AAYFSEAMSA RLLNSCLGIY
3989  .......... .......... .......... .......... ..........
12398 .......... .......... .......... .......... ..........
4871  EQLVKAAEVI ESDTCLAQGIL ARLNQQLSS PVGKPLERAA FYFKEALNNL
11846 .......... .......... .......... .......... ..........
2504  .......... .......... .......... .......... ..........
3935  .......... .......... .......... .......... ..........
11261 .......... .......... .......... .......... ..........
713   .......... .......... .......... .......... ..........
10964 .......... .......... .......... .......... ..........
23196 VSVDDRRTAN EMLRQIREHS SPLGNGSERL AHYFANSLEA RLAGTGTQIY
Tf1   IQQNNLTLAE ALVKQIGCLA VSQAGAMRKV ATYFAEALAR RIYRLSPPQN
Tf4   VQKENLTVAE ALVKQIGFLA VSQIGAMRQV ATYFAEALAR RIYRLSPSQS
18310 .......... .......... .......... .......... ..........
18652 .......... .......... .......... .......... ..........
4818  .......... .......... .......... .......... ........GT
21729 VMEIATAIAE GKTEIATEIL ARVSQTPNLE RNSEEKLVDF MVAALRSRIA
1110  ...LSMVNEL RQIVSIQGDP SQRIAAYMVE GLAARMAASG KFIYRALKCK
174   .......... .......... .......... .......... ..........
      301                                                  350
```

FIG. 15J

```
                                    |<--- Motif III (SCR VHIID) ---
  Scr  AALPSRWMPQ THSLKMVSAF QVFNGISPLV KFSHFTANQA IQEAFEKEDS
 3989  .......... .......... .......... ..LYRNKALL DEIGGMATSC
12398  .......... .......... .......... .......... ..........
 4871  LHNVSQTLSA CSLIFKVAAY KSFSEISPVL QFANFTSNQA LLESFHGFHR
11846  .......... .......... .......... .......... ..........
 2504  .......... .......... .......... .......... ..........
 3935  .......... .......... .......... .......... ...AMEGEKM
11261  .......... .......... .......... .......... ..........
  713  .......... .......... .......... .......... ..........
10964  .......... .......... .......... .......... ..........
23196  TALS...SKK TSAADMLKAY QTYMSVCPFK KAAIIFANHS MMRFTANANT
  Tf1  QIDHCLSDT. ........LQ MHFYETCPYL KFAHFTANQA ILEAFEGKKR
  Tf4  PIDHSLSDT. ........LQ MHFYETCPYL KFAHFTANQA ILEAFQGKKR
18310  .......... .......... .......... ........HA SVKGYN...H
18652  .......... .......... .......... ......ANVE ILEAIAGETR
 4818  SPTGPELLT. ........YM HILYEACPYF KFGYESANGA IAEAVKNESF
21729  SPVTELYGKE HLISTQL... ..LYELSPCF KLGFEAANLA ILDAADNNDGGMMI
 1110  EPPSDERLA. ........AM QVLFEVCPCF KFGFLAANGA ILEAIKGEEE
  174  .......... .......... .......... .......... ..........
       351                                                  400
```

FIG. 15K

```
      -- Motif III (VHIID) ---------------->|<- -- Motif IV ---
  Scr VHIIDLDIMQ GLQWPGLFHI LASRPGGPPH VRLTGLGTSM EA......LQ
 3989 IHVIDFDLGV GGQWASFLQE LAHRRGAGGM ALPLLKLTAF MSTASHHPLE LH
12398 .......... .......... .......... .......... ..........
 4871 LHIIDFDIGY GGQWASLMQE LVLRDNAAPLSLKITVFASPA NHVQLELG..
11846 .......... .......... .......... .......... ..........
 2504 .......... .......... .......... .......... ..........
 3935 VHVIDLDASE PAQWLALLQA FNSRPEGPPH LRITGVHHQK EVLE......
11261 .......... .......... .......... .......... ..........
  713 .......... .......... .......... .......... ..........
10964 .......... .......... .......... .......... ..........
23196 IHIIDFGISY GFQWPALIHRLSLSRPGGSPK LRITGIELPQ RGFRPAE...
  Tf1 VHVIDFSMNQ GLQWPALMQA LALREGGPPT FRLTGIGPPA PDNSDHLH..
  Tf4 VHVIDFSMSQ GLQWPALMQA LALRPGGPPV FRLTGIGPPA PDNFDYLH..
18310 VHIIDFSLMQ GLQWPALMDV FSAREGGPPK LRITGIGPNP IGGRDELH..
18652 VHIIDFQIAQ GSQYMFLIQE LAKRPGG... ...PPLLRVT GVDDSQSTYARGGGLS
 4818 VHIIDFQISQ GGQWVSLIRA LGARPGG... ...PPNVRIT GIDDPRSSFARQGGLE
 1110 VHIIDFDINQ GNQYMTLIRS IAELPGK... ...RPRLRLT GIDDPESVQRSIGGLR
21729 PHVIDFDIGE GGQYVNLLRT LSTRRNGKSQ SQNSPVVKIT AVANNVYGDCLVDDGGEERLK
  174 .......... .......... .......... .......... ..........
      401                                                   450
```

FIG. 15L

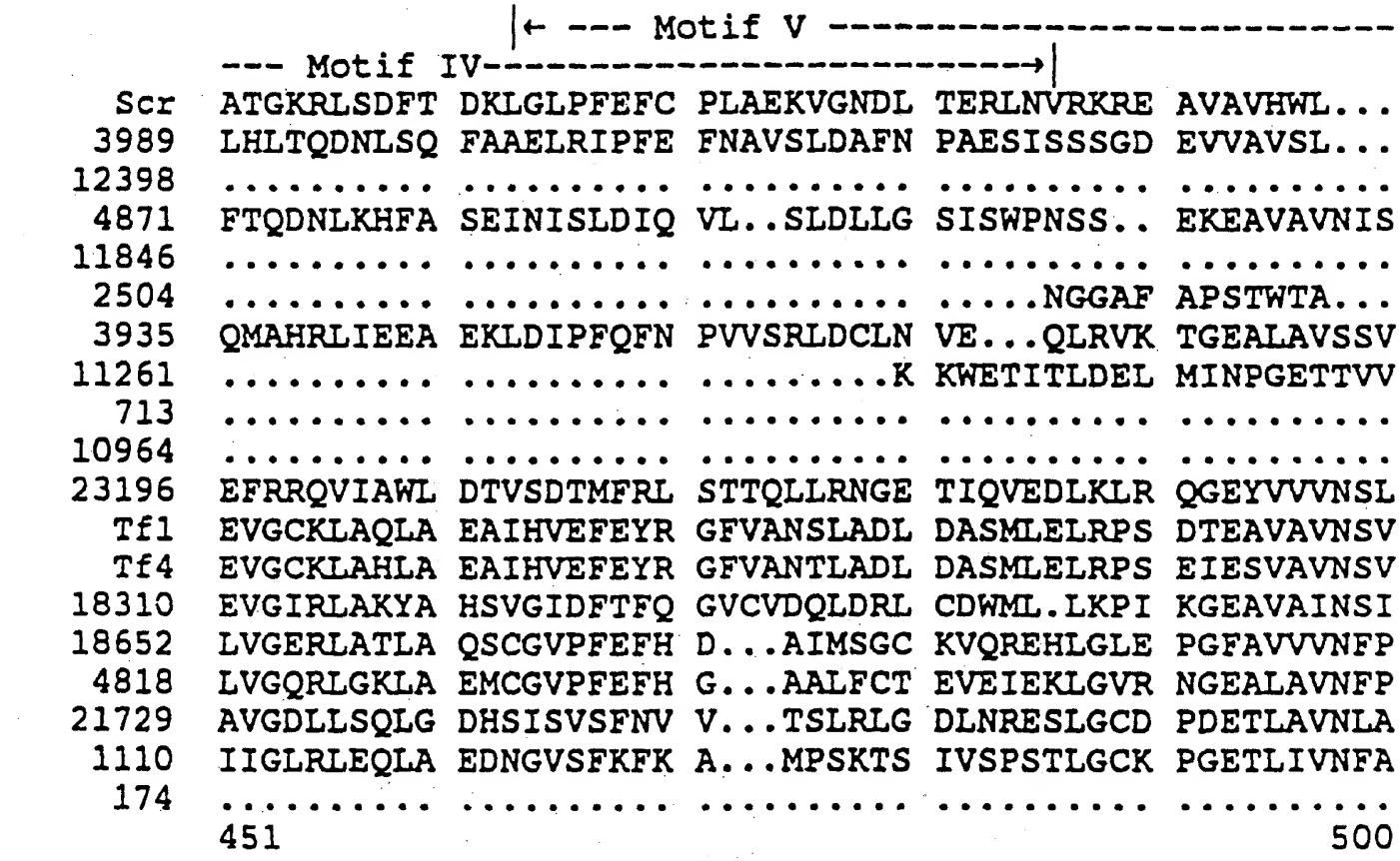


FIG. 15M

```
        ----- Motif V ------------------------------------------
  Scr   ...QHS.... ......... ......... ......... .........
 3989   .........P VG..... ......... ......... .........
12398   ......... ......... ......... ......... .........
 4871   .....AA... ......... ......... ......... .........
11846   ......... ......... ......... ......... .........
 2504   .........R SL..... ......... ......... .........
 3935   LQLHTFLASD DDLMRKNCAL RFHNNPSGVD LQRVLMMSHG SAAEARENDM
11261   NCIHRLQYTP DE..... ......... ......... .........
  713   ......... ......... ......... ......... .........
10964   ......... ......... ......... ......... .........
23196   FRFRNLL... DE..... ......... ......... .........
  Tf1   FELHKLLGRX GG..... ......... ......... .........
  Tf4   FELHKLLGRP GA..... ......... ......... .........
18310   LQLHRLLVDP DA..... ......... ......... .........
18652   YVLHHM...P DE..... ......... ......... .........
 4818   LVLHHM...P DE..... ......... ......... .........
21729   FKLYRV...P DE..... ......... ......... .........
 1110   FQLHHM...P DE..... ......... ......... .........
  174   ......... ......... ......... ......... .........
        501                                             550
```

FIG. 15N

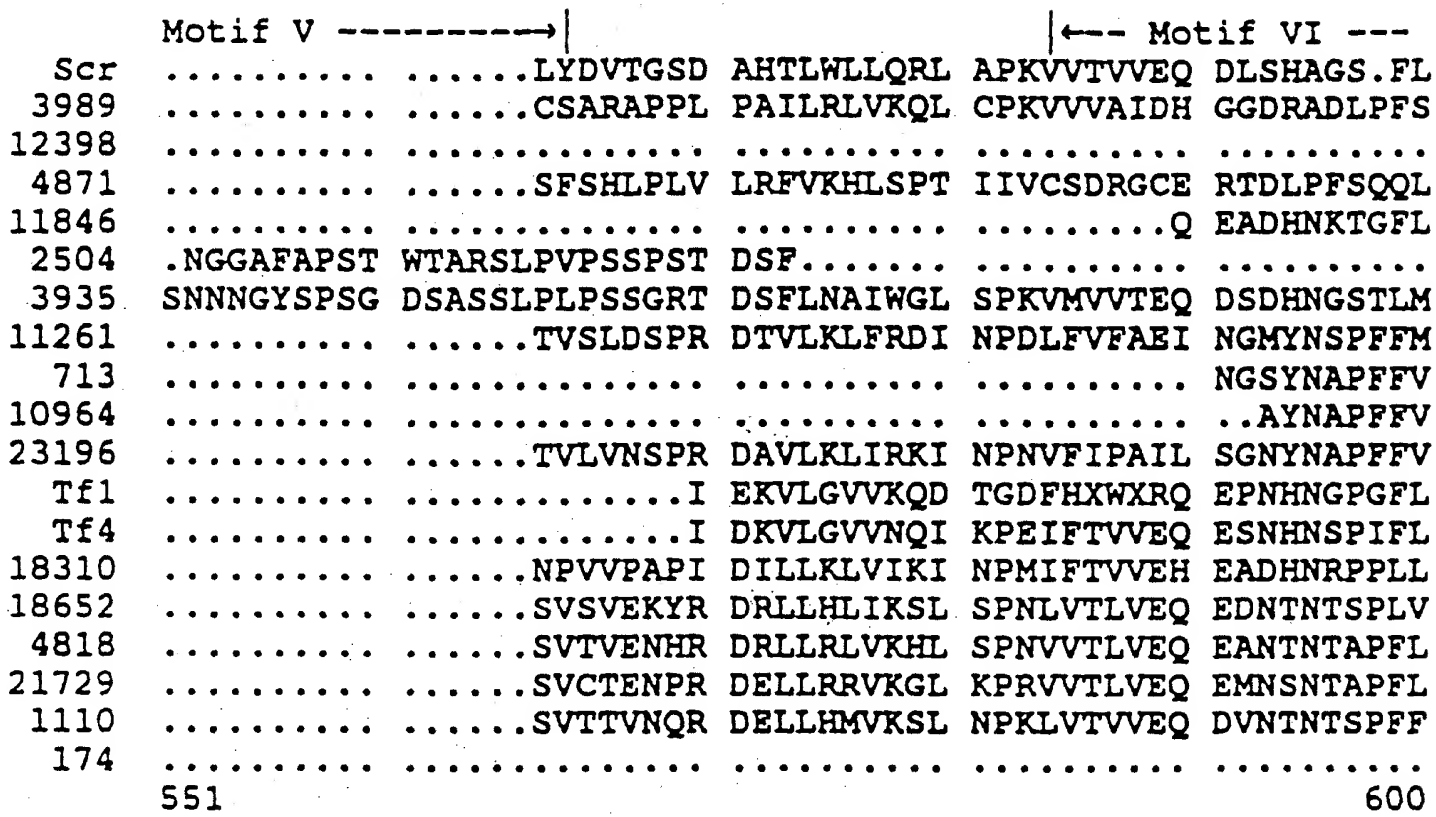


FIG. 150


```
        ------- Motif VI ----------------------------------------
  Scr   GRFVEAIHYY SALFDSLGAS Y..GEESEER HVVEQQLLSK EIRNVLAVGG
 3989   QHFLNCFQSC VFLDSLDAAG I..DADSA.. CKIERFLIQP RVEDAVIG..
12398   .......... .....SLEPN L..DRDSKER LRVERVLFGR RIMDLVRSDD
 4871   AHSLHSHTAL FESLDAVNAN L..DAM.... QKIERFLIQP EIEKLVLD..
11846   DRFTEALFYY SAVFDSLDAA N..NNNNNNN QRMEAEYLQR EICDIVCGEG
 2504   .......... .......... .......... .......... ..........
 3935   ERLLESLYTY AALFDCLETK V..PRTSQDR IKVEKMLFGE EIKNIISCEG
11261   TRFREALFHY SSLFDMFDTT IHAEDEYKNR SLLERELLVR DAMRVISCEG
  713   TRFREALFHY SAIFDMLETN I..PKDNEQR LLIESALFSR E.XNVISCEG
10964   TRFREALFHF SSIFDMLETI V..PREDEER MFLEMEVFGR EALNVIACEG
23196   TRFREALFHY SAVFDMCDSK L..AREDEMR LMYVFEFYGR EIVNVVASEG
  Tf1   DGXTESLHYY STXFDSLEGX ...PNSQD.. KLMSEXYLGX QICNLVACEG
  Tf4   DRFTESLHYY STLFDSLEGV ...PSGQD.. KVMSEVYLGK QICNVVACDG
18310   ERFTNALFHY ATMFDSLEAM HRCTSGRDIT DSLTEVYLRG EIFDIVCGEG
18652   SRFVETLDYY TAMFESIDAA R..PRDDKQR ISAEQHCVAR DIVNMIACEE
 4818   PRFVETMNHY LAVFESIDVK L..ARDHKER INVEQHCLAR EVENLIACEG
21729   GRVSESCACY GALLESVEST V..PSTNSDR AKVE.EGIGR KLVNAVACEG
 1110   PRFIEAYEYY SAVFESLDMT L..PRESQER MNVERQCLAR DIVNIVACEG
  174   .......... .RXFDSLEHD A..SKGEPRE DERGRXCLAR NIVNIVXCKX
        601                                                  650
```

FIG.15P

```
  Scr  PSRSGEVKF. .....ESWRE KMQQCGFKGI SLAG..NAAT QATLLLGMFP
 3989  .RHKA..Q.. ...KAIAWRS VFAATGFKPV QLSN..LAEA QADCLLKRVQ
12398  DNNKPGTRFG LMEEKEQWRV LMEKAGFEPV KPSN..YAVS QAKLLLWNYN
 4871  .RSRPIER.. ...PMMTWQA MFLQMGFSPV THSN..FTES QAECLVQRTP
11846  AARXERHE.. ...PLSRWRD RLTRAGLSAV PLG....SNA ..........
 2504  .......... .......... .......... .......... ..........
 3935  FERRERHE.. ...KLEKWSQ RIDLAGFGNV PLSY..YAML QARRLLQGCG
11261  AERFARPE.. ...TYKQWRV RILRAGFKPA TIS....KQI MKEAKEIVRK
  713  LERMERPE.. ...TYKQWQV RNQRVGFKQL PLN....QDM MKRARXEGQV
10964  WERVERPE.. ...TYKQWHV RAMRSGLVQV PFD....PSI MKTSLHKVHT
23196  TERVESRE.. ...TYKQWQA RLIRAGFRQL PLE....KEL MQNLKLKIEN
  Tf1  PDRVERHE.. ...TLSQWGN RFGSSGLAPA HLGS...NAF KQASMLLSVF
  Tf4  PDRVERHE.. ...TLSQWRN RFGSAGFAAA HIGS...NAF KQASMLLALF
18310  SARTERHE.. ...LFGHWRE RLTYAGLTQV WFDPDEVDTL KDQLIHVTSL
18652  SERVERHE.. ...VLGKWRV RMMMAGFTGW PVSTSAAFAA SE....MLK.
 4818  VEREERHE.. ...PLGKWRS RFHMAGFKPY PLSSYVNATI KG....LLE.
21729  IDRIERCE.. ...VFGKWRM RMSMAGFELM PLSEKIAESM KS....RGNR
 1110  EERIERYE.. ...AAGKWRA RMMMAGFNPK PMSAKVTNNI QN....LIKQ
  174  EERIERYE.. ...VTGKWRA RMMMAGFSPR PMSGRVTSNI ES....LIKR
       651                                                  700
```

FIG. 15Q

```
      ----- Motif VI ------------------>|
  Scr .SDGYTLVD. DNGTLKLGWK DLSLLTASAW TPRSX..... ..........
 3989 VRGFH..VEK RGAALTLYWQ RGELVSISSW RCX....... ..........
12398 YSTLYSLVES EPGFISLAWN NVPLLTVSSW RX........ ..........
 4871 VRGFH..VEE KHNSLLLCWQ RTELVGVSAW RCRSSX.... ..........
11846 .......... .......... .......... .......... ..........
 2504 .......... .......... .......... .......... ..........
 3935 FDGYR..IKE ESGCAVICWQ DRPLYSVSAW RCRKX..... ..........
11261 RYHRDFVIDS DNNWMLQGWK GRVIYAFSCW KPAEKFTNNN LNIX......
  713 LPTRTFIIDE DNRWLLQGWK GRILFALSTW KPDNRSSSX. ..........
10964 FYHKDFVIDQ DNRWLLQGWK GRTVMALSVW KPESX..... ..........
23196 GYDKNFDVDQ NGNWLLQGWK GRIVYASSLW VPSSSX.... ..........
  Tf1 NSGQGYRVEE SNGCLMLGWH TRPLITTSAW KLSTAAHX.. ..........
  Tf4 NGGEGYRVEE SDGCLMLGWH TRPLIATSAW KLSTNX.... ..........
18310 .SGSGFNILV CDGSLALAWH NRPLYVATAW CVTGGNAASS MVGNICKGTN
18652 AYDKNYKLGG HEGALYLFWK RRPMATCSVW KPNPNYIGX. ..........
 4818 SYSEKYTLEE RDGALYLGWK NQPLITSCAW RX........ ..........
21729 VHPG.FTVKE DNGGVCFGWM GRALTVASAW RX........ ..........
 1110 QYCNKYKLKE EMGELHFCWE EKSLIVASAW RX........ ..........
  174 DYCSKYKVKE EMGELHFSWE EKSLIVASAW SX........ ..........
      701                                                  750
```

FIG. 15R

```
Scr     .......... ....
3989    .......... ....
12398   .......... ....
4871    .......... ....
11846   .......... ....
2504    .......... ....
3935    .......... ....
11261   .......... ....
713     .......... ....
10964   .......... ....
23196   .......... ....
Tf1     .......... ....
Tf4     .......... ....
18310   DSRRKENRNG PMEX
18652   .......... ....
4818    .......... ....
21729   .......... ....
1110    .......... ....
174     .......... ....
          751          764
```

FIG. 15S

SRPa1 (1110)

CTTTGTCAATGGTAAATGAGCTGAGGCAGATAGTTTCTATCCAAGGAGACCCTTCTCAGA
GAATCGCAGCTTACATGGTGGAAGGTCTAGCTGCAAGAATGGCCGCTTCAGGAAAATTCA
TCTACAGAGCATTGAAATGCAAAGAGCCTCCTTCGGATGAGAGGCTTGCAGCTATGCAAG
TCCTGTTTGAAGTCTGCCCTTGTTTCAAGTTCGGGTTTTTAGCAGCTAATGGTGCGATAC
TTGAAGCAATCAAAGGTGAAGAAGAAGTTCACATAATCGATTTCGATATAAACCAAGGGA
ACCAATACATGACACTGATACGAAGCATTGCTGAGTTGCCTGGTAAACGACCTCGCCTGA
GGTTAACAGGAATTGATGACCCTGAATCAGTCCAACGCTCCATTGGAGGGCTAAGAATCA
TCGGTCTAAGACTCGAGCAACTCGCAGAGGATAATGGAGTATCCTTCAAATTCAAAGCAA
TGCCTTCAAAGACTTCGATTGTCTCTCCATCAACACTCGGTTGCAAACCAGGAGAAACCT
TAATAGTGAACTTTGCATTCCAACTTCACCACATGCCTGACGAGAGTGTCACAACAGTAA
ACCAGCGGGACGAGCTACTTCACATGGTCAAAAGCTTAAACCCAAAGCTTGTCACGGTCG
TTGAACAAGACGTGAACACAAACACTTCACCGTTCTTTCCCAGATTCATAGAGGCTTACG
AATACTACTCAGCAGTTTTCGAGTCTCTAGACATGACACTTCCAAGAGAAAGCCAAGAGA
GGATGAATGTAGAAAGACAGTGTCTCGCTAGAGACATAGTCAACATTGTTGCTTGCGAAG
GAGAAGAACGGATAGAGAGATACGAGGCTGCGGGAAAATGGAGAGCAAGGATGATGATGG
CTGGATTCAATCCAAAACCAATGAGTGCTAAAGTAACCAACAATATACAAAACCTGATAA
AGCAACAATATTGCAATAAGTACAAGCTTAAAGAAGAAATGGGTGAGCTCCATTTTTGCT
GGGAGGAGAAAAGCTTAATCGTTGCTTCAGCTTGGAGGTAAGATAAGTGACAAGAGCATA
TAGTCTTTATGTTTCATAAAACATAATTATGTTTTTACTGTAATCTTGGGTTATTGTGTA
ACTGGTTAAATCATCTCCATGTATTATTACCAGAGGTTAGGGGTGATCACAGGTACTAAA
AGCTAATCTAACACTTATGGAAGAATTTTTCTTTCTTTTTTTTCCCTATTATATAAAAAT
AATTAGAGTTTTGGTTCTAAACCTATTTGCTAAGTGTGAATGAGTCTTTACATGTTCATA
TTTCAGTTCAAATGGTTAAATTTGTTAAGGTTCTCACTTAAAAAAAAA

FIG. 16A

SRPa3 (3935)

GCTATGGAAGGAGAGAAGATGGTTCATGTGATTGATCTCGATGCTTCTGAGCCAGCTCAA
TGGCTTGCTTTGCTTCAAGCTTTTAACTCTAGGCCTGAAGGTCCACCTCATTTGAGAATC
ACTGGTGTTCATCACCAGAAGGAAGTGCTTGAACAAATGGCTCATAGACTCATTGAGGAA
GCAGAGAAACTCGATATCCCGTTTCAGTTTAATCCCGTTGTGAGTAGGTTAGACTGTTTA
AATGTAGAACAGTTGCGGGTTAAAACAGGAGAGGCCTTAGCCGTTAGCTCGGTTCTTCAA
TTGCATACCTTCTTGGCCTCTGATGATGATCTCATGAGAAAGAACTGCGCTTTACGGTTT
CAGAACAACCCTAGTGGAGTTGACTTGCAGAGAGTTCTAATGATGAGCCATGGCTCTGCA
GCTGAGGCACGTGAGAATGATATGAGTAACAACAATGGGTATAGCCCTAGCGGTGACTCG
GCCTCATCTTTGCCTTTACCAAGTTCAGGAAGGACTGATAGCTTCCTCAATGCTATTTGG
GGTTTGTCTCCAAAGGTCATGGTGGTCACTGAGCAAGACTCAGACCACAACGGCTCCACA
CTAATGGAGAGGCTATTAGAATCACTTTACACCTACGCAGCATTGTTTGATTGCTTGGAA
ACAAAAGTTCCAAGAACGTCTCAAGATAGGATCAAAGTGGAGAAGATGCTCTTCGGGGAG
GAGATCAAGAACATCATATCCTGCGAGGGATTTGAGAGAAGAGAAAGACACGAGAAGCTT
GAGAAATGGAGCCAGAGGATCGATTTGGCTGGTTTTGGGAATGTTCCTCTTAGCTATTAT
GCGATGTTGCAGGCTAGGAGATTGCTTCAAGGGTGCGGTTTTGATGGGTATAGAATCAAG
GAAGAGAGCGGGTGCGCAGTAATTTGCTGGCAAGATCGACCTCTATACTCGGTATCAGCT
TGGAGATGCAGGAAGTGAATGATATATTACAGTTTGTCTTCTATTTTGGTTATGAGCAGA
GTCCCTTTCTTTTTTGTATACATGGGGACACAATCTTAGTTGTTTTGTGATGGTGACTTT
CTGTCTCTTTATGCTATTTTGGCTTAAATGCTTCTACTGCCTCTGCATGTAAAGCCTTTG
TGTGTTGGTTCAATTTGGTCTGGTGTGGGTGTAATACCAAACCAAATCCAATTTGAGCTG
AAGATAACTAATTTGATGATCGGCTCGTGCC

FIG. 16B

SRPa4 (4818)

GGCACGAGCCCAACGGGTCCTGAGCTTCTTACTTATATGCATATCTTGTATGAAGCCTGC
CCTTATTTCAAATTCGGTTATGAATCTGCTAATGGAGCTATAGCTGAAGCTGTGAAGAAC
GAAAGTTTTGTGCACATTATCGATTTCCAGATTTCTCAAGGTGGTCAATGGGTGAGTTTG
ATCCGTGCTCTTGGTGCTAGACCTGGTGGACCTCCGAACGTTAGGATAACGGGAATTGAT
GATCCGAGATCATCGTTTGCTCGTCAAGGAGGACTTGAGTTAGTTGGACAAAGACTTGGG
AAGCTAGCTGAAATGTGCGGTGTTCCGTTTGAGTTCCATGGAGCTGCTTTATGCTGCACG
GAAGTCGAAATCGAGAAGCTAGGAGTTAGAAATGGAGAAGCGCTCGCGGTTAACTTCCCG
CTTGTTCTTCACCACATGCCTGATGAGAGTGTAACTGTGGAGAATCACAGAGATAGATTG
TTGAGATTGGTCAAACACTTGTCACCAAACGTTGTGACTCTGGTTGAGCAAGAAGCGAAT
ACAAACACTGCGCCGTTTCTTCCCCGGTTTGTCGAGACAATGAACCATTACTTGGCAGTT
TTCGAATCAATAGATGTGAAACTCGCTAGAGATCACAAGGAAAGGATCAATGTTGAGCAG
CATTGTTTGGCTAGAGAGGTTGTGAATCTTATAGCTTGTGAAGGTGTTGAAAGAGAAGAG
AGGCACGAGCCACTAGGGAAATGGAGGTCTCGGTTTCACATGGCGGGATTTAAACCGTAT
CCTTTGAGCTCGTATGTGAACGCAACAATCAAAGGATTGCTTGAGAGTTATTCAGAGAAG
TATACACTTGAAGAAAGAGATGGAGCATTGTATTTAGGATGGAAGAATCAACCTCTTATC
ACTTCTTGTGCTTGGAGGTAACTAATAAAAACCTTGTTCGGTTTCAGAAGAGATTAGAAA
CTTCTTTTAAAGTTTGCAGAATCTGTTTGTAAAAGTAAAACTCATGCATGATCCGNAGGA
ACAAGTTGTCAAATGTTGTAGTAGTAAGTGATATGTTGATGACCCAAAAAAAAAAAAAAA
AAAAA

FIG. 16C

SRPa5 (4871)

GCGGCTATCTTCTACGGCCACCACCACCATACACCTCCGCCGGCAAAGCGGCTCAACCCT
GGTCCCGTGGGGATAACAGAGCAGCTGGTTAAGGCAGCAGAGGTCATAGAGAGCGACACG
TGTCTAGCTCAGGGGATATTGGCGCGGCTCAATCAACAGCTCTCTTCTCCCGTCGGGAAG
CCATTAGAAAGAGCAGCTTTTTACTTCAAAGAAGCTCTCAATAATCTCCTTCACAACGTC
TCCCAAACCCTAAACCCTTATTCCCTCATCTTCAAGATCGCTGCTTACAAATCCTTCTCA
GAGATCTCTCCCGTTCTTCAGTTCGCCAACTTTACCTCCAACCAAGCCCTCTTAGAGTCC
TTCCATGGCTTCCACCGTCTCCACATCATCGACTTCGATATCGGCTACGGTGGCCAATGG
GCTTCCCTCATGCAAGAGCTTGTTCTCCGCGACAACGCCGCTCCTCTCTCCCTCAAGATC
ACCGTTTTCGCTTCTCCGGCGAACCACGACCAGCTCGAACTTGGCTTCACTCAAGACAAC
CTCAAGCACTTCGCCTCTGAGATCAACATCTCCCTTGACATCCAAGTTTTGAGCTTAGAC
CTCCTCGGCTCCATCTCGTGGCCTAACTCGTCGGAGAAAGAAGCTGTCGCCGTTAACATC
TCCGCCGCGTCCTTCTCGCACCTCCCTTTGGTCCTCCGTTTCGTGAAGCATCTATCTCCG
ACGATCATCGTCTGCTCCGACAGAGGATGCGAGAGGACGGATCTGCCCTTCTCTCAACAG
CTCGCCCACTCGCTGCACTCACACACCGCTCTCTTCGAATCCCTCGACGCCGTCAACGCC
AACCTCGACGCAATGCAGAAGATCGAGAGGTTTCTTATACAGCCGGAGATAGAGAAGCTG
GTGTTGGATCGTAGCCGTCCGATAGAAAGGCCGATGATGACGTGGCAAGCGATGTTTCTA
CAGATGGGTTTCTCACCGGTGACGCACAGTAACTTCACGGAGTCTCAAGCCGAGTGTTTA
GTCCAACGGACGCCAGTGAGAGGCTTTCACGTCGAGAAGAAACATAACTCACTTCTCCTA
TGTTGGCAAAGGACAGAACTCGTCGGAGTTTCAGCATGGAGATGTCGCTCCTCCTGATTT
CCACCGGAGTTTCAATTATTAAAAAAATATTTTCCTTAATTCAATTTATCTTAAATGACA
AATTTTTAGTTTCTGATTTTATTTTGCTCAGTGCGATGGATTTTTAAATTTAAGTTTCAC
ACAAATATATAAATTTTTG

FIG. 16D

SRPa6 (12398)

AATCGCTTGAACCGAATTTGGATCGAGATTCGAAAGAAAGGCTGAGAGTGGAGAGAGTGC
TGTTCGGTAGGAGGATTATGGATTTGGTCCGATCAGATGATGATAATAATAAACCGGGAA
CCCGGTTTGGGTTAATGGAGGAGAAAGAACAATGGAGAGTGTTGATGGAGAAAGCTGGAT
TTGAGCCGGTTAAACCGAGTAATTACGCGGTTAGCCAAGCGAAGCTGCTACTATGGAACT
ACAATTATAGTACATTGTATTCACTTGTTGAATCGGAGCCAGGTTTCATCTCCTTGGCTT
GGAACAATGTGCCTCTCCTCACCGTTTCCTCTTGGCGTTGACTACTTGGTCCGATAAGTT
AATCTAGTATTTTGAGTTAGCTTTTAGAATTGAATTGTTTGGGGTTAGATTTGGATGTTT
AATTAGTCTCTAGCCTATTCTCTTACTCTTTTTTGTCTAGTGCTTGGAGTGATGATGGTT
TGTCGTTTATGTTCATTTGTAATATATATTGTATGTAACATTTGACTAAAAAAAAAAAAA
AAAAAAAA

FIG. 16E

SRPa7 (21729/3635/17410)

AAAGACTTTAGCAGATTTTCAAGCGGCTCAGAACATCAACAACAACAACAACAACCG
TTTTATAGTCAAGCAGCTCTCAACGCTTTTCTTTCAAGGTCTGTGAAGCCTCGAAATTAT
CAGAATTTTCAATCTCCGTCGGCCGATGATTGATCTCACGTCGGTGAATGATATGAGTTT
GTTTGGTGGTTCTGGTTCATCTCAGCGTTACGGTTTACCGGTTCCCAGGTCTCAGACGCA
ACAGCAACAATCGGATTACGGTTTATTTGGTGGGATCCGAATGGGAATCGGGTCGGGTAT
TAATAATTATCCAACATTAACCGGCGTTCCGTGTATTGAACCGGTTCAAAACCGGGTTCA
TGAATCGGAGAACATGTTGAATAGTTTAAGAGAGCTTGAGAAACAGCTTTTAGATGATGA
CGATGAGAGTGGTGGTGATGATGACGTGTCAGTTATAACAAATTCAAATTCCGATTGGAT
TCAAAATCTCGTGACTCCGAACCCGAACCCGAACCCGGTTTTGTCTTTTTCACCGAGCTC
TTCTTCTTCGTCTTCTTCGCCTTCTACAGCTTCGACGACGACATCGGTATGTTCTAGGCA
AACGGTTATGGAAATCGCGACGGCGATCGCGGAAGGGAAAACAGAGATAGCGACGGAGAT
TTTGGCGCGTGTTTCTCAAACGCCTAATCTTGAGAGGAATTCAGAGGAGAAGCTTGTTGA
TTTCATGGTGGCTGCGCTTCGATCGAGGATAGCTTCTCCAGTGACGGAATTGTATGGGAA
GGAGCATTTAATCTCGACTCAATTGCTCTACGAGCTCTCTCCTTGTTTCAAACTCGGTTT
CGAGGCCGCGAATCTCGCCATTCTCGACGCCGCCGATAACAACGACGGTGGAATGATGAT
ACCGCACGTTATCGATTTCGATATCGGAGAAGGTGGACAATACGTTAACCTTCTCCGTAC
ATTATCCACGCGCCGGAATGGTAAAAGTCAGAGTCAGAATTCTCCGGTGGTTAAGATCAC
CGCCGTGGCGAACAACGTTTACGGATGTTTAGTCGATGACGGTGGAGAAGAGAGGTTAAA
AGCCGTCGGAGATTTGTTGAGCCAACTCGGTGATCGACTCGGTATCTCCGTAAGTTTCAA
CGTGGTGACGAGTTTACGACTCGGTGATCTGAATCGTGAATCTCTCGGGTGTGATCCCGA
CGAGACTTTGGCTGTGAACTTAGCTTTCAAGCTTTATCGTGTTCCCGACGAAAGCGTATG
CACGGAGAATCCAAGAGACGAACTTCTCCGGCGCGTGAAGGGACTTAAACCGCGCGTGGT
TACTCTAGTGGAGCAAGAAATGAATTCGAATACGGCGCCGTTTTTAGGGAGAGTGAGTGA
GTCATGCGCGTGTTACGGTGCGTTGCTTGAGTCGGTCGAGTCTACGGTTCCTAGTACGAA
TTCCGACCGTGCCAAAGTTGAGGAAGGAATTGGCCGGAAGCTAGTAAACGCGGTGGCGTG
CGAAGGAATCGATCGTATAGAGCGGTGCGAGGTGTTCGGGAAATGGCGAATGCGGATGAG
CATGGCTGGGTTTGAGTTAATGCCATTGAGTGAGAAGATAGCGGAGTCGATGAAGAGTCG

FIG. 16F-1

TGGAAACCGAGTCCACCCGGGCTTTACCGTTAAAGAAGATAACGGAGGTGTGTGCTTTGG
TTGGATGGGACGGGCACTCACTGTCGCATCCGCTTGGCGTTAACTTCACACACTCTTTTT
TTTCTTCTTATTATTACCATATTATTATTAATTTTCGAGATTATTCTGATATTATTATCA
TTGTGATTTTCCGTTTCGAAAAGTGTAGGAATCTTATGTAACAAAGAAAAAAAAAAGACT
TTTATGTTTTTCTAATAATAAAAGAAAGAGTGATTGGGTTCAAAAAAAAAAAAAAAAAAA
AAAAAAAA

FIG.16F-2

SRPa8 (10964)

TGCATACAACGCACCGTTTTTCGTAACACGGTTTCGCGAAGCTCTATTTCATTTCTCCTC
GATTTTTGACATGCTTGAGACAATTGTGCCACGAGAAGACGAAGAGAGGATGTTCCTTGA
GATGGAGGTCTTTGGGAGAGAGGCACTGAATGTGATTGCTTGCGAAGGTTGGGAAAGAGT
GGAGAGGCCTGAGACATACAAGCAGTGGCACGTACGGGCTATGAGGTCAGGGTTGGTGCA
GGTTCCATTTGACCCAAGCATTATGAAGACATCGCTGCATAAGGTCCACACATTCTACCA
CAAGGATTTTGTGATCGATCAAGATAACCGGTGGCTCTTGCAAGGCTGGAAGGGAAGAAC
TGTCATGGCTCTTTCTGTTTGGAAACCAGAGTCCAAGGCTTGACCGAGAAATCCTCGTTG
GCATATGAGAGACCATCTCTTGATTTTCTTCCTGTGTAATTCCCAGAGACAGAATTACAG
ATGTAAGAAGAGAATGCTGCACAAAGAACTTGTTCAAAGATAATATTGATGTAAGTCCTG
TTTTATAACTTTCTAGCTGTGTTTTTGTTGTTTCTCAGCTAGATTCTCCTAACGGTATTC
TTGTAGCTAGGGTGATCAGATTGTTTGTATATTGCTAGCAGAGTTAGTTTGTCTAGATTG
TAACACATATAAGAGGAAGCTTAGAGTTTCTATGGTTTAAAGAGAAGTTTTTTCCTTCTC
CAATGTAAAAAAAAAAAAAAAAAA

FIG. 16G

SRPa10 (11261)

AAAAAATGGGAAACCATCACTCTTGATGAACTTATGATCAATCCAGGAGAGACAACGGTC
GTCAACTGCATTCATCGGTTACAATACACTCCTGATGAAACTGTGTCATTAGACTCTCCA
AGAGACACGGTTCTGAAGCTATTCAGAGATATCAATCCTGACCTCTTTGTGTTTGCAGAG
ATTAACGGAATGTACAACTCTCCTTTCTTCATGACGAGGTTCCGAGAAGCGCTTTTTCAT
TACTCTTCACTCTTTGACATGTTTGACACCACAATACACGCAGAGGATGAGTACAAAAAC
AGGTCACTGTTGGAGAGAGAGTTACTTGTGAGAGACGCGATGAGCGTGATTTCCTGCGAG
GGTGCAGAGCGGTTTGCGAGGCCTGAAACCTACAAGCAATGGCGAGTTAGGATTTTGAGA
GCCGGGTTTAAGCCAGCAACTATTAGCAAACAGATCATGAAGGAGGCTAAGGAAATTGTG
AGGAAACGTTACCATAGAGATTTTGTGATCGATAGCGATAACAATTGGATGCTTCAAGGA
TGGAAAGGAAGAGTCATCTATGCTTTTTCTTGCTGGAAACCTGCTGAGAAGTTCACAAAC
AATAATTTAAACATCTGAAAAATGTTACTTCTCAATTACATCATTTTTGTTTCCCAATGG
TTTTGTAGAATATGTTTGATCCCGTGAGTGGATGCAACTCTTTTTTCCTGCAAGTACATA
TTGTATTCAAATCCTTGTGGAAATGATAAATTGTTTAATCAAAAAAAAAAAAAAA

FIG. 16H

SRPa11 (18652)

GCGAATGTTGAGATCTTGGAAGCAATAGCTGGGGAAACCAGAGTCCACATTATCGATTTT
CAGATTGCACAGGGATCACAATACATGTTTTTGATTCAGGAGCTTGCGAAACGCCCTGGT
GGGCCGCCGTTGCTGCGTGTGACGGGTGTGGATGATTCACAGTCCACCTATGCTCGTGGG
GGAGGACTCAGCTTGGTAGGTGAGAGGCTTGCAACTTTGGCGCAGTCATGTGGTGTCCCG
TTTGAGTTTCACGATGCCATCATGTCTGGGTGCAAGGTGCAGCGGGAACATCTCGGGTTG
GAACCTGGCTTTGCTGTTGTTGTGAACTTCCCATATGTATTACACCACATGCCAGACGAG
AGCGTAAGTGTTGAAAAATACAGAGACAGGCTGCTGCATCTGATCAAGAGCCTCTCCCCA
AAACTGGTTACTCTAGTAGAGCAAGAATCCAACACAAACACCTCGCCATTGGTGTCACGG
TTTGTGGAAACACTGGATTACTACACAGCGATGTTTGAGTCGATAGATGCAGCACGGCCA
CGGGATGATAAGCAGAGAATCAGCGCAGAACAACACTGTGTAGCAAGAGACATAGTGAAC
ATGATAGCATGTGAGGAGTCAGAGAGAGTAGAGAGACACGAGGTACTGGGGAAATGGAGG
GTCAGAATGATGATGGCTGGGTTCACGGGTTGGCCGGTCAGCACATCTGCAGCGTTTGCA
GCGAGTGAGATGCTGAAAGCTTATGACAAAAACTACAAACTGGGAGGCCATGAAGGAGCG
CTCTACCTCTTCTGGAAGAGACGACCCATGGCTACATGTTCCGTGTGGAAGCCAAACCCA
AACTATATTGGGTAAGTTATAGTGATGATGGTTACTTGAGTGGATAAAGAAGAGCACAAC
AAAAACACATCTGTCGCTGTAAATTTTTTAGGATGTGCAATGATGTTTTAAGTTGTAACA
CAACCTAAGTTATATATGTATACAAACCAAACCTGGTGGTTGTTTTTCTCTTGTAAATTG
TCATGTGGTTGTGGGTGGGAAGCTAGTAATGAAATATAACCAAAACATTGATTAGGTCAA
AAAAAAAAAAAA

FIG. 16I

SRPa12 (23196)*

TCTTACTCAAGGTTCTTCTTTGTCATCTTGTTGCCGAATCCACAAAGAGGAGAATAAAGA
TTCGACCTTTATTAGATATTAACGACTCTGGATTTTTGGGTTTTTGGAGTTGGATCCACA
TGGGTTCTTATCCGGATGGATTCCCTGGATCCATGGACGAGTTGGATTTCAATAAGGACT
TTGATTTGCCTCCCTCCTCAAACCAAACCTTAGGTTTAGCTAATGGGTTCTATTTAGATG
ACTTAGATTTCTCATCCTTGGATCCTCCAGAGGCATATCCCTCCCAGAACAACAACAACA
ACAACATCAACAACAAAGCTGTAGCAGGAGATCTGTTATCATCTTCATCTGATGACGCTG
ATTTCTCTGATTCTGTTTTGAAGTATATAAGCCAAGTTCTTATGGAAGAGGATATGGAAG
AGAAGCCTTGTATGTTTCATGATGCTTTGGCTCTTCAAGCTGCTGAGAAATCTCTCTATG
AGGCTCTTGGTGAGAAAGACCCTTCTTCGTCTTCTGCTTCTTCTGTGGATCATCCTGAGA
GATTGGCTAGTCATAGCCCTGACGGTTCTTGTTCAGGTGGTGCTTTTAGTGATTACGCTA
GCACCACTACCACTACTTCCTCTGATTCTCACTGGAGTGTTGATGGTTTGGAGAATAGAC
CTTCTTGGTTACATACACCTATGCCGAGTAATTTTGTTTTCCAGTCTACTTCTAGGTCCA
ACAGTGTCACCGGTGGTGGTGGTGGTGGTAATAGTGCGGTTTACGGTTCAGGTTTTGGCG
ATGATTTGGTTTCGAATATGTTTAAAGATGATGAATTGGCTATGCAGTTCAAGAAAGGGG
TTGAGGAAGCTAGTAAGTTCCTTCCTAAGTCTTCTCAGCTCTTTATTGATGTGGATAGTT
ACATCCCTATGAATTCTGGTTCCAAGGAAAATGGTTCTGAGGTTTTTGTTAAGACGGAGA
AGAAAGATGAGACAGAGCATCATCATCATCATAGCTATGCACCACCACCCAACAGATTAA
CTGGTAAGAAAAGCCATTGGCGCGACGAAGATGAAGATTTCGTTGAAGAAAGAAGTAACA
AGCAATCAGCTGTTTATGTTGAGGAAAGCGAGCTTTCTGAAATGTTTGATAACATGTTCC
TATGTGGCCCTGGGAAACCTGTATGCATTCTTAACCAGAACTTTCCTACAGAATCCGCTA
AAGTCGTGACCGCACAGTCAAATGGAGCAAAGATTCGTGGGAAGAAATCAACTTCTACTA
GTCATAGTAACGATTCTAAGAAAGAAACTGCTGATTTGAGGACTCTTTTGGTGTTATGTG
CACAAGCTGTATCAGTGGATGATCGTAGAACCGCCAACGTTTAGCTAAGGCAGATACGAG
AGCATTCTTCGCCTCTAGGCAATGGTTCAGAGCGGTTGGCTCATTATTTTGCAAATAGTC
TTGAAGCACGCTTAGCTGGGACCGGTACACAGATCTACACCGCTTTATCTTCGAAGAAAA
CGTCTGCAGCAGACATGTTGAAGGCTTACCAGACATACATGTCGGTCTGCCCTTTCAAGA
AAGCTGCTATCATATTTGCTAACCACAGCATGATGCGTTTCACTGCAAACGCCAACACGA
TCCACATAATAGATTTCGGAATATCTTACGGTTTTCAGTGGCCTGCTCTGATTCATCGCC
TCTCGCTCAGCAGACCTGGTGGTTCGCCTAAGCTTCGAATTACCGGTNNNNNNNNNNNN

FIG.16J-1

NNNNNNNNNNNNNNNNNNNNNNNGAGTTCAGGAGACAGGTCATCGCTTGGCTCGATACT
GTCAGCGACACAATGTTCCGTTTGAGTACAACGCAATTGCTCAGAAATGGGGAAACGATC
CAAGTCGAAGACTTAAAGCTTCGACAAGGAGAGTATGTGGTTGTGAACTCTTTGTTCCGT
TTCAGGAACCTTCTAGATGAGACCGTTCTGGTAAACAGCCCGAGAGATGCAGTTTTGAAG
CTGATAAGAAAAATAAACCCGAATGTCTTCATTCCAGCGATCTTAAGCGGGAATTACAAC
GCGCCATTCTTTGTCACGAGGTTCAGAGAAGCGTTGTTTCATTACTCGGCTGTGTTTGAT
ATGTGTGACTCGAAGCTAGCTAGGGAAGACGAGATGAGGCTGATGTATGTGTTTGAGTTT
TATGGGAGAGAGATTGTGAATGTTGTGGCTTCTGAAGGAACAGAGAGAGTGGAGAGCCGA
GAGACATATAAGCAGTGGCAGGCGAGACTGATCCGAGCCGGATTTAGACAGCTTCCGCTT
GAGAAGGAACTGATGCAGAATCTGAAGTTGAAAATCGAAAACGGGTACGATAAAAACTTC
GATGTTGATCAAAACGGTAACTGGTTACTTCAAGGGTGGAAAGGTAGAATCGTGTATGCT
TCATCTCTATGGGTTCCTTCGTCTTCATAGATGTTGTTTCTTACGTTCTAAGCGACTGGG
ATTTATGTAGGGCTTTTCTGTTGATAGTCTCTCGCCAACACGAGTGGATTAAGTTCAGAG
TTAGGGTTCTTGAACACTAGAATGTTGTTATATTATGCTTGTGACATAGCGTGTGTAAGA
GTGTAGCCTAAGAGATATAGTACTCATTGCATGATCTTTTGCTATATGTTNCATGT

FIG. 16J-2

SRPd1

TCTGCAGACAATTTTNAGGAGGCCAATACCATGCTATTGGAAATTTCAGAACTG
TCCACACCTNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGTACTTCTCAGAGGN
AATGTCGGNNAGATTAGTTAGCTCCTGCTTAGGAATCTATGCTTCTCTTCCNGC
AACAGTGGTGCCTCCTCATGGTCAGAAAGTGGCCTCA

FIG. 16K

SRPg1

TCAACTGAGAATCTAGAAGATGCCAACAAGATGCTTCTGGAGATTTCTCAGTTA
TCAACACCGTTCNNCACTTCAGCACAGCGTGTGGCAGCATATTTCTCAGAAGCC
ATATCAGCAAGGTTGGTGAGTTCATGTCTAGGGATATACGCAACTTTGCCACAC
ACACACCAAAGCCACAAGGTAGCTTCAGCTTTTCAAGTGTTCAATGGTATTAGT
CCTTTAGTGGAGTTCTCACACTTCACAGCAAACCAAGCAATTCAAGAAGCCTTC
GAAAGAGAAGAGAGGGTGCACATCATAGATCTTGATATAATGCAAGGGTTG

FIG. 16L

SRPp1

TCTGCAGACAACTTTGAAGAAGCCAATACAATACTGCCTCAGATCACAGAACTC
TCCACCCCCTATNGCAACTCGGTGCAACGAGTGGCTGCCTATNNNNNNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNTGCATAGGAATGTATTCTCCTCTCCCTCCT
ATTCACATGTCCCAGAGCCAGAAAATTGTGAAT

FIG. 16M

Partial DNA sequence of *ZCARECROW* gene

GATATCAGCATCATCAATTTTAAATGTAAGTTGGCAAAAGATCATGAGGGTTCTCATAGT
AATTTGGCCACAAGGTATGACACTGTCTCAATTGAGCAATCTAGTAGAGAAACTGATCCA
TCATATATTGCTCATATTGAAAGTGAAAAAGATATGCTCAAGAACCTAGTAGAGAAGCTA
AAAATTGAAAAATCTAGCTCTACTAGAAAAATATGATAGGTTGCCTGTTTCTCATGAAAA
TTTATTAGATAATCATATCATGGCTAGATGTCGCTCATGAGGTTGTTCTTGCTAGTTTAG
ATTCCTGTGGGCATTCATCTCTTTTAGATGCACTAACATGATAGGAAGTTTCTAATCTGG
TGCTTCACAATTCTGGTGATTCATGCTTCCTTCATTGCAATTGATATTGATGCTTGATTC
ATGCTTCAGTCACTTTGTGCGTTTAATTGGTATTGTATGTATCACTAGATTGTAGGGTGT
CTGCAACTAGTGTTTCACCATGTGGTTTTTTAGTATCATTCGTATTAGTTTCTAACTTTC
TATTGATATATTAAAGTGATAACTAGTTTTAGAAATATTCTCTTGTGCCATTAATGCTAC
AACTTGTTTTTAGCGTGTACGTTAGCATTATAATATTTCCTTATTATGAAAGCGGAAGAG
AAACGCGCCCAACCAGAGCATCCACGTCGTCTCATTTCACCTTCATCGTTGGATCATAGA
TGAGCGGTCCACGGTGAACTCCGTTTGCCTGCAAAACCACGTCCTCTACGCGCTGTTAAG
TAGCTTCTAGAAACATCACGATGTGTCCCGTCCATTCCTTTAGGAGGAGCCGGATCCGGC
GCCGCAGTCGCCCAAGGTCCCGACCGCCGCGGCCTCGGCCGCCGCCGCCAAGGAGCGGAA
GGAGGTGCAGCGGCGGAAGCAGCGCGACGAGGAGGGCCTCCACCTGCTGAGTGCTGACGC
TGCTGCTGCAGTGCGCGGAGGCCGTGAACGCGGACAACCTCGACGACGCGCACCAGACGC
TGCTGGAGATCGCGGAGCTGGCCACGCCGTTCGGCACCTCGACCCAGCGCGTGGCCGCCT
ACTTCGCGGAGGCCATGTCGGCGCGCGTCGTCAGCTCCTGCCTAGGCCTGTACGCGCCGC
TGCCGCCGGGCTCCCCCGCCGCGGCGCGCCTCCACGGCCGCGTGGCCGCCGCGTTCCAGG
TGTTCAACGGCATCAGCCCCTTCGTCAAGTTCTCGCACTTCACCGCCAACCAGGCCATCC
AGGAGGCGTTCGAGCGGGAGGAGCGTGTGCACATCATCGACCTCGACATCATGCAGGGGC
TGCAGTGGCCGGGCCTCTTCCACATCCTTGTCTCCCGCCCCGGCGGCCCGCCCAGGGTCA
GGCTCACCGGCCTGGGGGCGTCCATGGACGCGCTCGAGGCGACGGGGAAGCGCCTCTCCG
ACTTCGCCGACACGCTCGGCCTGCCCTTCGAGTTCTGCGCCGTCGCCGAGAAGGCCGGCA
ACGTTGACCCGCAGAAGCTGGGCGTCACGCGGCGGGAGGCCGTCGCCGTCCACTGGCCGC
ACCACTCGCTTTACGACGTCATCGGCTCCGACTCCAACACGCTCTGGCTCATCCAAAGGT
CCTCCATTTTCCTTCTCTGCCTTTCTTCCATGTCAAATCTTGATGCAATCATGACCACTT
TTCAGCTGCTGACATTGGATAATGTGAGCTTTACGGCAAGCATCAAGTCGTGGTAGTACA

FIG. 17A-1

TCCATTACAGCTATTTCTAAAATATTCTTCGGAGGTTTCCTGCTCATAGTAAAAAAAAAT
CGCGTTTTGAAGCTCAAAAGGCGATTTCTTCCGAGGTTTGCTGTTGAGCGCTATTTTGGA
AACCCCATTTTCTCAATTGATTTTTATTTTTTAAAGAAAAATTAGTTCATTTTTCTCTTG
TGAAATGGAGTCCCAAACTAACCCTAATATTAAAAAAAACGCGCTTTGGAGCTCAAAACG
CTCGTTGTTATGACCAACCAGCTTTATAGGTTTAAAAAGGTTGAATCTTGACAATGCTTT
TGAAAAGGTTGAATCTTGACAATGCTTTTGAGATGATACTGTAGTGTAGTCTGTAGTGGA
GCATCCTCCATGGTCTTTGGTGATCGAGAATTCCTGCAGCCCGGGGGATCC

FIG. 17A-2

Partial amino acid sequence of ZCARECROW protein

YQHHQFXMXVGKRSXGFSXXFGHKVXHCLNXAIXXRNXSIIYCSYXKXKRYAQEPSREAK
NXKIXLYXKNMIGCLFLMKIYXIIISWLDVAHEVVLASLDSCGHSSLLDALTXXEVSNLV
LHNSGDSCFLHCNXYXCLIHASVTLCVXLVLYVSLDCRVSATSVSPCGFLVSFVLVSNFL
LIYXSDNXFXKYSLVPLMLQLVFSVYVSIIIFPYYESGRETRPTRASTSSHFTFIVGSXM
SGPRXTPFACKTTSSTRCXVASRNITMCPVHSFRRSRIRRRSRPRSRPPRPRPPPPRSGR
RCSGGSSATRRASTCXVLTLLLQCAEAVNADNLDDAHQTLLEIAELATPFGTSTQRVAAY
FAEAMSARVVSSCLGLYAPLPPGSPAAARLHGRVAAAFQVFNGISPFVKFSHFTANQAIQ
EAFEREERVHIIDLDIMQGLQWPGLFHILVSRPGGPPRVRLTGLGASMDALEATGKRLSD
FADTLGLPFEFCAVAEKAGNVDPQKLGVTRREAVAVHWPHHSLYDVIGSDSNTLWLIQRS
SIFLLCLSSMSNLDAIMTTFQLLTLDNVSFTASIKSWXYIHYSYFXNILRRFPAHSKKKS
RFEAQKAISSEVCCXALFWKPHFLNXFLFFKEKLVHFSLVKWSPKLTLILKKTRFGAQNA
RCYDQPALXVXKGXILTMLLKRLNLDNAFEMILXCSLXWSILHGLWXSRIPAARGI

FIG. 17B

```
          302                                                  349
SCR       SADNLEEANKLLLEISQLSTPYGTSAQRVAAYFSEAMSARLLNSCLGI
SRPd1     SADNFxEANTMLLEISELSTPxxxxxxxxxxYFSxxMSxRLVSSxLxI
SRPg1     STENLEDANKMLLEISQLSTGxxxxxxxxxxxxxxxxxxxxxxxxSCLGI
SRPp1     SADNFEEANTILPQITELSTPYxNSVGRVAAYxxxxxxxxxxxxCIGM

          350                                                  396
SCR       YAALPSRWMPQTH-SLKMVSAFQVFNGISPLVKFSHFTANQAIQEAFE
SRPd1     YASLPATVVP--PHGQKVAS
SRPg1     YATLP-----HTHQSHKVASAFQVFNGISPLVEFSHFTANQAIQEAFE
SRPp1     YSPLPPIxMSQ---SQKIVN

          397          412
SCR       KEDSVHIIDLDIMQGL
SRPg1     REERVHIIDLDIMQGL
```

FIG. 18

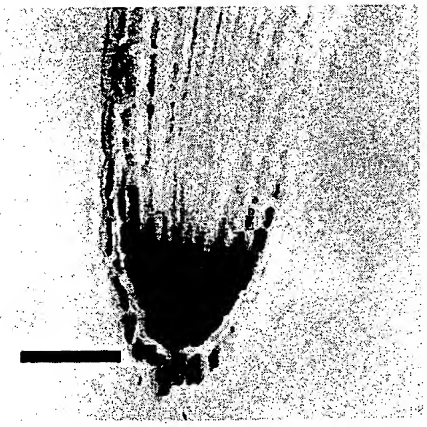


FIG.19A

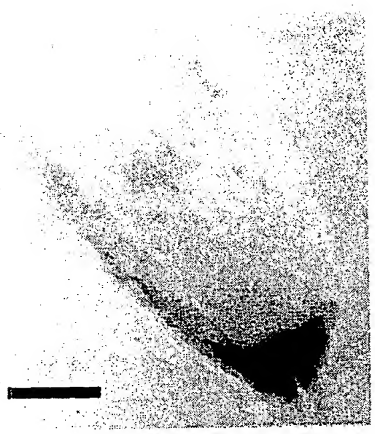


FIG.19C

FIG.19B

FIG.19D

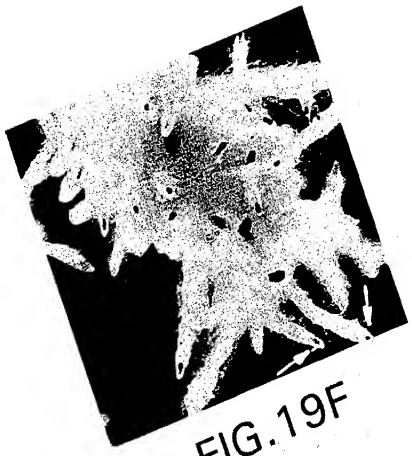


FIG.19F

FIG.19E

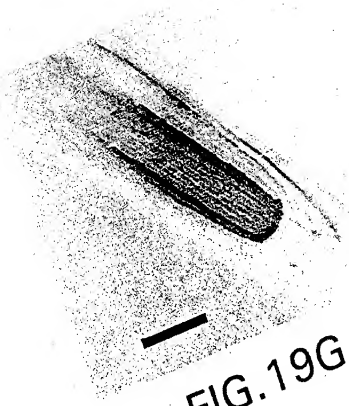


FIG.19G

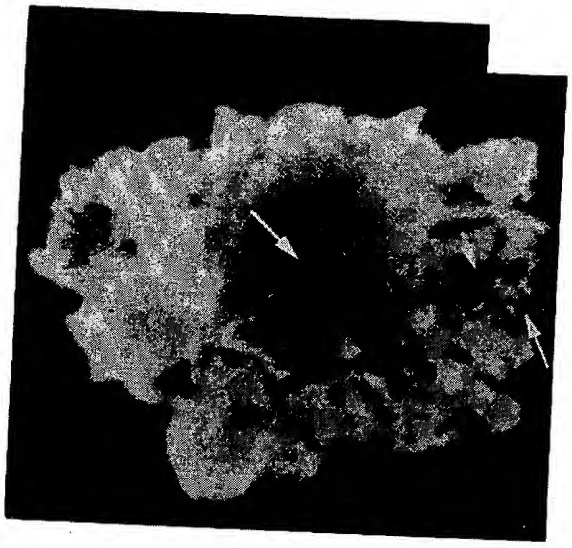


FIG.20A

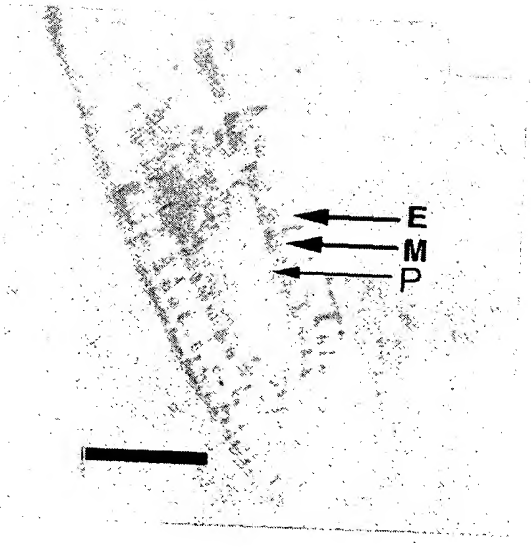


FIG.20B

SCR Promoter::GUS

FIG.21A

SCR Promoter::SCR

FIG.21B

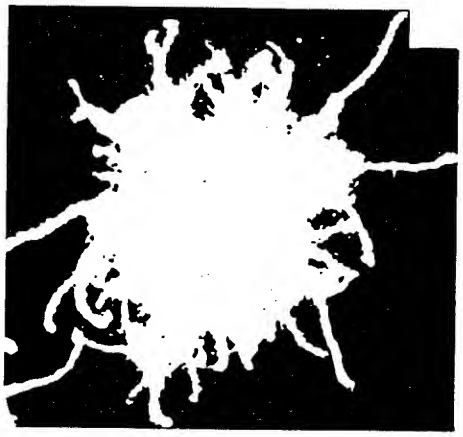


FIG.21C

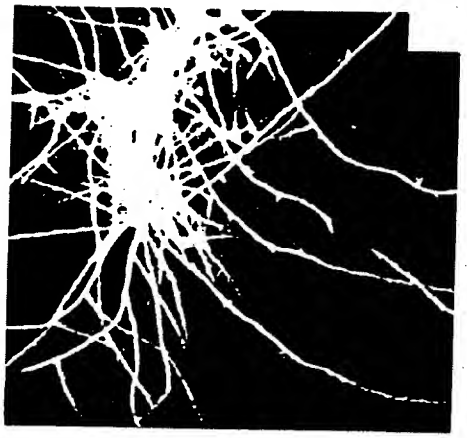


FIG.21D

FIG.21E

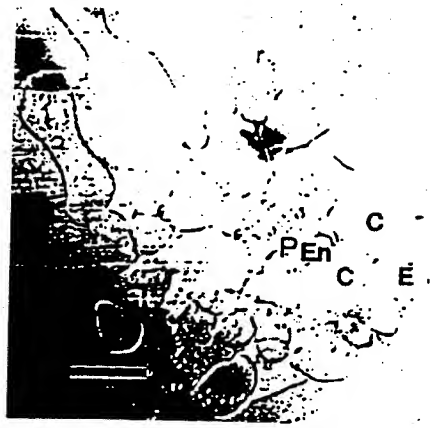
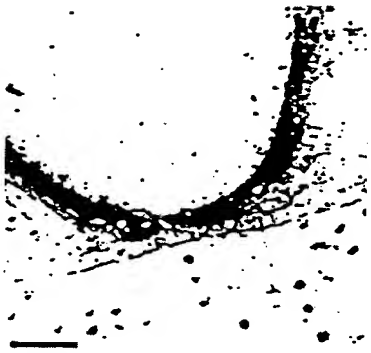


FIG.21F

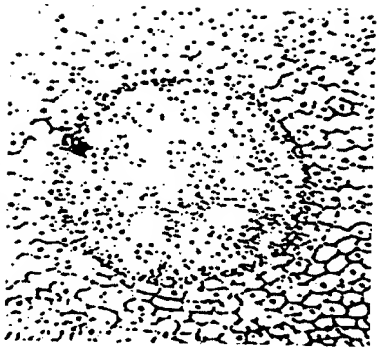
Maize primary root

FIG.22A



Maize primary root

FIG.22B



Maize primary root

FIG.22C

Maize embryo

FIG.22D

FIG.22E

Maize lateral root

FIG.22F

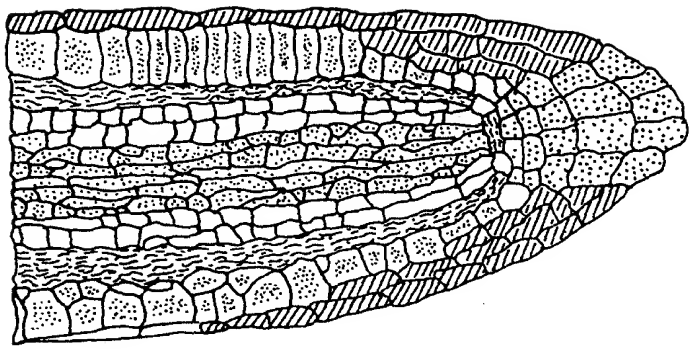


FIG.23B

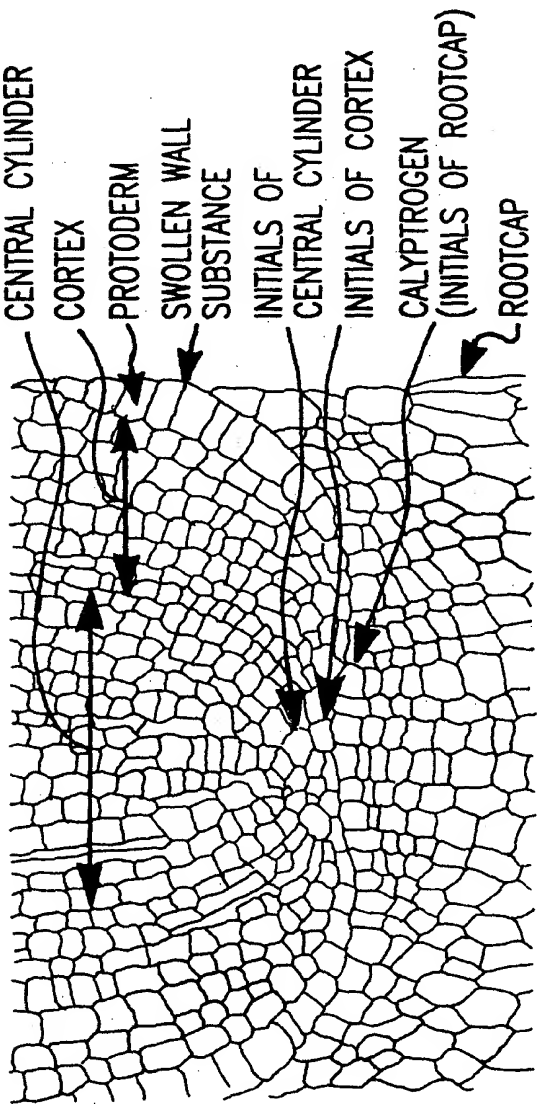


FIG.23A

FIG.24A

FIG.24B

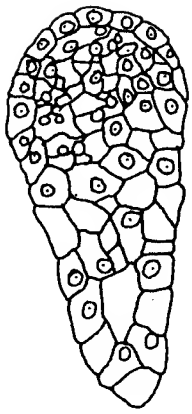


FIG.24C

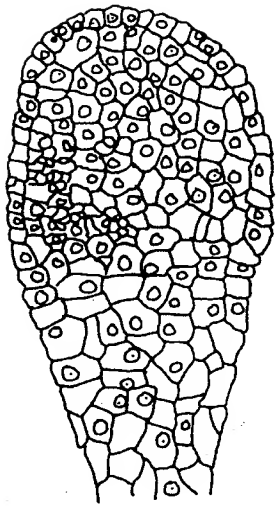


FIG.24D

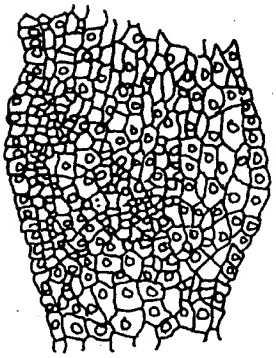


FIG.24E

FIG.24F

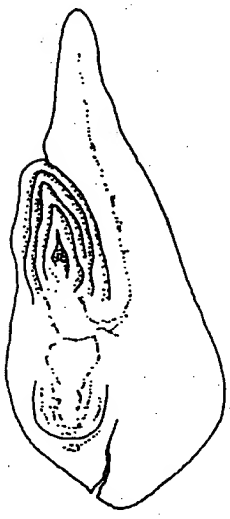


FIG.24G

```
    ctgctagctcagcctactcactccactcaactcacccccaactccactccgctcccgagc   60
    ccggactgactgactgactgtggtggtggtggtgcatcagcagcccgcgcggcgccaaaa  120
    cacgcaaactgctccctccctcactcacccctatcccccgcgctgggtcgcccgatcgcc  180
    atgcgcgcggcggcttcctcttggcgtttctagatgggctcctcctcctccctcctcttc  240
    tcctcgtcctcctccgccgcatccaccgccccccactcctttccccactctcATGCCACC  300
1                                                       M  P  P
    GCCACCGCCTCCGCCTCCTCTCACTCCTTATTGCCGCCGCTGCCCTCCCCCACACCTCCC  360
4     P  P  P  P  P  P  L  T  P  Y  C  R  R  C  P  P  P  H  L  P
    TCCGCCTCCTCCTTCTTCCCCAAACCACTTCCTCCTCCACTACCTCCATCAGCTAGACCA  420
24    P  P  P  P  S  S  P  N  H  F  L  L  H  Y  L  H  Q  L  D  H
    CCAAGAAGCCGCCGCCGCCGCCATGGTCCGCAAGCGCCCCGCGTCCGACATGGACCTCCC  480
44    Q  E  A  A  A  A  A  M  V  R  K  R  P  A  S  D  M  D  L  P
    GCCGCCGCGCCGCCACGTCACGGGCGACCTCTCCGACGTCACGGCGGCCGCTGCCGCCGG  540
64    P  P  R  R  H  V  T  G  D  L  S  D  V  T  A  A  A  A  A  G
    TGTTGGTGGTAGTGGCGCGCCGTCCTCCGCCAGCGCGCAGCTGCCCGCGCTGCCCACCCA  600
84    V  G  G  S  G  A  P  S  S  A  S  A  Q  L  P  A  L  P  T  Q
    GCTCCACCAGCTGCCCCCCGCGTTCCAGCACCACGCGCCGGAGGTGGACGTGCCCGCGCA  660
104   L  H  Q  L  P  P  A  F  Q  H  H  A  P  E  V  D  V  P  A  H
    CCCGGCCCCGGCCGCCCACGCGCAGGCGGGCGGCGAGGCAACCGCGTCCACGACCGCGTG  720
124   P  A  P  A  A  H  A  Q  A  G  G  E  A  T  A  S  T  T  A  W
    GGTGGACGGCATCATCCGCGACATCATCGGGAGCAGCGGCGGCGCCGCGGTCTCCATCAC  780
144   V  D  G  I  I  R  D  I  I  G  S  S  G  G  A  A  V  S  I  T
    GCAGCTCATCCACAACGTCCGCGAGATCATCCACCCCTGCAACCCCGGCCTCGCGTCGCT  840
164   Q  L  I  H  N  V  R  E  I  I  H  P  C  N  P  G  L  A  S  L
    CCTGGAGCTCCGCCTCCGCTCCCTCCTCGCAGCCGACCCGGCCCCACTGCCGCCGCCGCC  900
184   L  E  L  R  L  R  S  L  L  A  A  D  P  A  P  L  P  P  P  P
    GCAGCCGCAGCAGCATGCTCTCCTGCACGGCGCTCCGGCCGCCGCTCCCGCGGGGCTGAC  960
204   Q  P  Q  Q  H  A  L  L  H  G  A  P  A  A  A  P  A  G  L  T
    GCTCCCTCCCCCGCCACCGCTTCCGGACAAGCGCCGCCACGAGCATCCACCGCCGTGCCA 1020
224   L  P  P  P  P  P  P  L  P  D  K  R  R  H  E  H  P  P  P  C  Q
    GCAGCAACAGCAGGAGGAACCGCATCCGGCGCCGCAGTCGCCCAAGGCCCCGACCGCGGA 1080
244   Q  Q  Q  Q  E  E  P  H  P  A  P  Q  S  P  K  A  P  T  A  E
    AGAGACCGCAGCGGCGGCCGCCGCCGCACAAGCAGCAGCTGCTGCGGCCGCCAAGGAGCG 1140
264   E  T  A  A  A  A  A  A  A  Q  A  A  A  A  A  A  A  K  E  R
    GAAGGAGGAGCAGCGGCGGAAGCAGCGCGACGAGGAGGGCCTCCACCTGCTGACGCTGCT 1200
284   K  E  E  Q  R  R  K  Q  R  D  E  E  G  L  H  L  L  T  L  L
    GCTGCAGTGCGCCGAGGCCGTGAACGCGGACAACCTGGACGACGCGCACCAGACGCTGCT 1260
304   L  Q  C  A  E  A  V  N  A  D  N  L  D  D  A  H  Q  T  L  L
```

FIG.25A

```
    GGAGATCGCGGAGCTAGCGACGCCGTTCGGCACCTCGACGCAGCGCGTGGCCGCCTACTT 1320
324   E  I  A  E  L  A  T  P  F  G  T  S  T  Q  R  V  A  A  Y  F
    CGCGGAGGCCATGTCGGCGCGGCTCGTCAGCTCCTGCCTGGGCCTGTACGCGCCGCTGCC 1380
344   A  E  A  M  S  A  R  L  V  S  S  C  L  G  L  Y  A  P  L  P
    GCCGGGCTCCCCCGCCGCGGCGCGCCTCCACGGCCGCGTCGCCGCCGCGTTCCAGGTGTT 1440
364   P  G  S  P  A  A  A  R  L  H  G  R  V  A  A  A  F  Q  V  F
    CAACGGCATCAGCCCCATTCGTCAAGTTCTCGCACTTCACCGCCAACCGGCCATCCAGGA 1500
384   N  G  I  S  P  F  V  K  F  S  H  F  T  A  N  Q  A  I  Q  E
    GGCGTTCGAGCGGGAGGAGCGCGTGCACATCATCGACCTCGACATCATGCAGGGGCTGCA 1560
404   A  F  E  R  E  E  R  V  H  I  I  D  L  D  I  M  Q  G  L  Q
    GTGGCCGGGGCTCTTCCACATCCTTGCCTCCCGCCCCGGGGGCCCGCCCAGGGTGAGGCT 1620
424   W  P  G  L  F  H  I  L  A  S  R  P  G  G  P  P  R  V  R  L
    CACCGGCCTCGGGGCGTCCATGGAGGCGCTCGAGGCCACGGGGAAGCGCCTCTCCGATTT 1680
444   T  G  L  G  A  S  M  E  A  L  E  A  T  G  K  R  L  S  D  F
    CGCCGACACGCTCGGCCTGCCCTTCGAGTTCTGCGCCGTCGCCGAGAAGGCCGGCAATGT 1740
464   A  D  T  L  G  L  P  F  E  F  C  A  V  A  E  K  A  G  N  V
    TGACCCGGAGAAGCTAGGGGTCACGAGGCGGGAGGCCGTCGCCGTCCACTGGCTGCACCA 1800
484   D  P  E  K  L  G  V  T  R  R  E  A  V  A  V  H  W  L  H  H
    CTCGCTCTACGACGTCACTGGCTCCGACTCCAACACGCTCTGGCTCATCCAAAGgtagga 1860
504   C  L  Y  D  V  T  G  S  D  S  N  T  L  W  L     I  Q  R
    aggagtacaccatctctcgatcctgacttccttgctaccatgtcaaatcttgatgcaatc 1920
    atggccacttttcagctactaacactttagtttagccaatgcgacatccagtacaactaa 1980
    tctaaaaaaataatcttcagaggtttcctagtaaaaaaaccgcgtttttggagctcaaaa 2040
    agcttgtcattatgaccaaccaactttctaggcttaaaaaggttgaatcttggcaatgct 2100
    tttgagacgatgctgtactgaagtactggtagagagagtatcctccatggcctttgttga 2160
    tcccagaaccacaaaagatagtatttcgctcgcatttggttagtggaggtgttctgatca 2220
    tcacttggaggatggagctgaaagttcctatcatcatgaccaactttccatggcaaaagg 2280
    tttctagttccaagtggcaggacgatgattactgagtgactgaatggagtaactgtcatc 2340
    ttctaccactaaccatcatttattaatacataaatcatcatccggagcctaaactcagaa 2400
    aggctaatcaaaagtgcaatctttctcaaatggctgccatatgccagtggtacatgcctg 2460
    gccattgtacttttcggtgaaccatctcgtctcaagcatgagatgaaggcctgaactgc 2520
    aatgtccttgatttgatgcaaccattattagaagaaacgctaagcgatgccggtcctggc 2580
    aagggcaatgccatatcgtcagacagacagggattcggaatcgaatggctagctggtgac 2640
    aaatcgcacggggattaataaactacattggtcattgattccatcccccacacacctgca 2700
```

FIG.25B

```
    gGCTGGCCCCCAAGGTGGTGACAATGGTGGAGCAGGACCTGAGCCACTCGGGCTCCTTCC 2760
522   L  A  P  K  V  V  T  M  V  E  Q  D  L  S  H  S  G  S  F
    TGGCGCGCTTCGTGGAGGCCATCCACTACTACTCGGCGCTGTTCGACTCGCTGGACGCGA 2820
541 L  A  R  F  V  E  A  I  H  Y  Y  S  A  L  F  D  S  L  D  A
    GCTACGGCGAGGACAGCCCCGAGCGGCACGTCGTGGAGCAGCAGCTGCTGTCGCGGGAGA 2880
561 S  Y  G  E  D  S  P  E  R  H  V  V  E  Q  Q  L  L  S  R  E
    TCCGCAACGTGCTGGCCGTGGGCGGGCCGGCCCGCACCGGCGACGTCAAGTTCGGCAGCT 2940
581 I  R  N  V  L  A  V  G  G  P  A  R  T  G  D  V  K  F  G  S
    GGCGCGAGAAGCTGGCGCAGTCCGGGTTCCGCGCCGCCTCGCTCGCCGGCAGCGCCGCGG 3000
601 W  R  E  K  L  A  Q  S  G  F  R  A  A  S  L  A  G  S  A  A
    CGCAGGCGTCCCTGCTGCTCGGCATGTTCCCCTCCGACGGGTACACGCTGGTGGAGGAGA 3060
621 A  Q  A  S  L  L  L  G  M  F  P  S  D  G  Y  T  L  V  E  E
    ACGGCGCGCTGAAGCTCGGGTGGAAGGACCTCTGCCTGCTCACCGCGTCGGCCTGGCGCC 3120
641 N  G  A  L  K  L  G  W  K  D  L  C  L  L  T  A  S  A  W  R
    CCATCCAGGTGCCGCCGTGCCGTTGAtgagacctctgcctgctcctgcttgcgttgagag 3180
661 P  I  Q  V  P  P  C  R  *
    gccgccactccacttgttttgcatctgtagctgctcggtttggtcatcagctgggagata 3240
    agaaaagcggaaacgtactaattgctctggagtagatccatccattcacagtgatagtta 3300
    ctgatgtactaagctttaattagttcaatgctagatcgttcttgttcaggtgtcgatcgc 3360
    gtatccttgtccttggtctccttttcattttggtgctttgtctagtcgctttcccgacta 3420
    atgccgtgctcttcatgcgcgttctagtgaagattcttgccgagaatattagcatagttt 3480
    tcatgtaaagtagccatcaagcaagtatta 3510
```

FIG.25C

```
          *                    *** *      **
Zm SCR    MPPPPPPPPL TPYCRRCPPP HLPPPPPSSP NHFLLHYLHQ LDGQEAAAAA    50
At SCR    MAES------ GDFNGGQPPP HSPLRTTSSG SSSSNN--RG PPPPPPPPLV    42

          ***** ** *    *             *          *      **  * *
Zm SCR    MVRKRPASDM DLPP---PRR HVTGDLSDVT AAAAAGVGGS GAPS-SASAQ    96
At SCR    MVRKRLASEM SSNPDYNNSS RPPRRVSHLL DSNYNTVTPQ QPPSLTAAAT    92

             *                                      *       ** * *
Zm SCR    LPALPTQLHQ LP--PAFQHH APEVDVPAHP APAAH-AQAG GEATASTTAW   143
At SCR    VSSQPNPPLS VCGFSGLPVF PSDRGGRNVM MSVQPMDQDS SSSSASPTVW   142

          ** **** *  **    ***  *** *** **  **** *  * ** *****
Zm SCR    VDGIIRDIIG SSGGAAVSIT QLIHNVREII HPSNPGLASL LELRLRSLLA   193
At SCR    VDAIIRDLIH SS--TSVSIP QLIQNVRDII FPCNPNLGAL LEYRLRSLML   190

           **      *  **    *                *              * **
Zm SCR    ADPAPLPPPP QPQQHALLHG APAAAPAGLT LPPPPPLPDK RRHEHPPPCQ   243
At SCR    LDPSS-SSDP SPQTFEPLYQ ISNNPSP--- -PQQQQQHQQ QQQQHKPPPP   235

            ** *          *  *    *   * *    * *  ** *** *   *
Zm SCR    QQQQEEPHPA PQSPKAPTAE ETAAAAAAAQ AAAAAAAKER KEEQRRKQRD   293
At SCR    PIQQQERENS STDA-PPQPE TVTATVPAVQ TNTAEALRER KEEIKRQKQD   284

          ********** ******* ** **  *   ** **  * ** * ** *******
Zm SCR    EEGLHLLTLL LQCAEAVNAD NLDDAHQTLL EIAELATPFG TSTQRVAAYF   343
At SCR    EEGLHLLTLL LQCAEAVSAD NLEEANKLLL EISQLSTPYG TSAQRVAAYF   334

           *******   **** ** **                  ***** ***** ****
Zm SCR    AEAMSARLVS SCLGLYAPLP PGSPAAARLH GRVAAAFQVF NGISPFVKFS   393
At SCR    SEAMSARLLN SCLGIYAALP SRWMPQTH-S LKMVSAFQVF NGISPLVKFS   383

          ********** *** *  *** ********** ********** ****** ***
Zm SCR    HFTANQAIQE AFEREERVHI IDLDIMQGLQ WPGLFHILAS RPGGPPRVRL   443
At SCR    HFTANQAIQE AFEKEDSVHI IDLDIMQGLQ WPGLFHILAS RPGGPPHVRL   433

          **** *****  *********  **** **** ***** **** *** **** *
Zm SCR    TGLGASMEAL EATGKRLSDF ADTLGLPFEF CAVAEKAGNV DPEKLGVTRR   493
At SCR    TGLGTSMEAL QATGKRLSDF TDKLGLPFEF CPLAEKVGNL DTERLNVRKR   483
```

FIG.26A-1

```
         ******** * *********   **** **** ***** **** *** **** *
Zm SCR   EAVAVHWLHH SLYDVTGSDS NTLWLIQRLA PKVVTMVEQD LSHSGSFLAR   543
At SCR   EAVAVHWLQH SLYDVTGSDA HTLWLLQRLA PKVVTVVEQD LSHAGSFLGR   533

         ********** ***** **** * * ****** ***** **** ******* *
Zm SCR   FVEAIHYYSA LFDSLDASYG EDSPERHVVE QQLLSREIRN VLAVGGPART   593
At SCR   FVEAIHYYSA LFDSLGASYG EESEERHVVE QQLLSKEIRN VLAVGGPSRS   583

         * *** **** *  * **    **** ** **  ********* *****  **
Zm SCR   GDVKFGSWRE KLAQSGFRAA SLAGSAAAQA SLLLGMFPSD GYTLVEENGA   643
At SCR   GEVKFESWRE KMQQCGFKGI SLAGNAATQA TLLLGMFPSD GYTLVDDNGT   633

         ******** * ****** *
Zm SCR   LKLGWKDLCL LTASAWRPIQ VPPCR   668
At SCR   LKLGWKDLSL LTASAWTPR- ----S   653
```

FIG.26A-2

FIG.27A

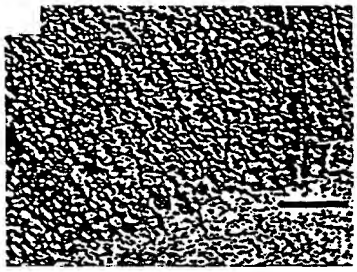


FIG.27B

FIG.27C

FIG.27D

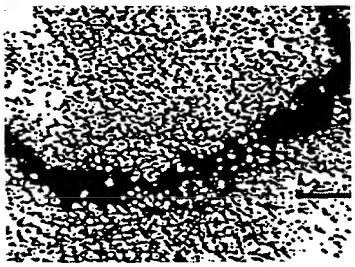
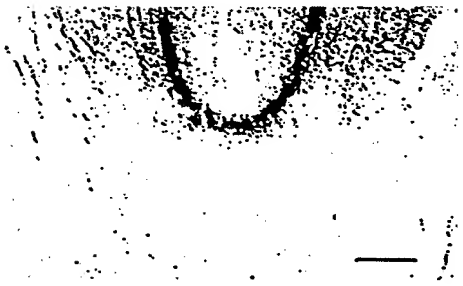


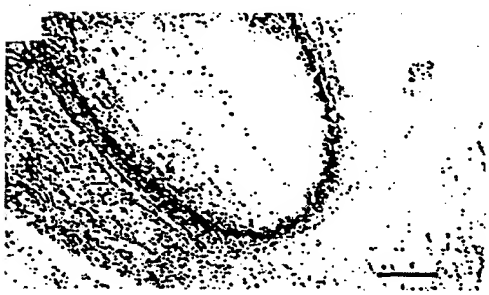
FIG.27E

FIG.27F



96H

FIG.27G



100H

FIG.27H

```
    ctttgtcaat ggtaaatgag ctgaggcaga tagtttctat ccaaggagac ccttctcaga
 61 gaatcgcagc ttacatggtg gaaggtctag ctgcaagaat ggccgcttca ggaaaattca
121 tctacagagc attgaaatgc aaagagcctc cttcggatga gaggcttgca gctatgagat
181 cctgtttgaa gtctgccctt gtttcaagtt cgggttttta gcagctaatg gtgcgatact
241 tgaagcaatc aaaggtgaag aagaagttca cataatcgat ttcgatataa accaagggaa
301 ccaatacatg acactgatac gaagcattgc tgagttngcc tgggtaaacg acctcgcctg
361 aggttaaaca ggaattgatg accctgaatc cagtnccaac cgctccattt gggggggcct
421 aaagaa
```

FIG.28

```
    gagtacgatc ttaaagctat tcccggtgac gcgattctca atcagttcgc tatcgattcg
 61 gcttcttcgt ctaaccaagg cggcggagga gatacgtata ctacaaacaa gcggttgaaa
121 tgctcaaacg gcgtcgtgga aaccactaca gcgacggctg agatcaactc ggcatgttgt
181 cctggttgac tcgcaggaga acggtgtgcg tctcgttcac gcgcttttgg cttgcgctga
241 aagctgttca gaaagagaat ctgactgtag cggantctgg tgaagcaaat cggattctta
301 gccgtttctc aaatcggagc gatgagaaaa gtcgctactt act
```

FIG.28A-1

```
    aaatttttca attacctaat ataatgaaag ataagatctt aacaagtgac aaagggaaaa
 61 acagtaggat ttagtttggc ttcggtcgga aatctatcat cataaccggt tcaacagatc
121 aattcattga gccaccatct aattggtgag agtttccaag ccgaggtggc tatgagcggt
181 cgtgtgtgcc aacccaacat gagacagccg tcactctcct ccacccgata accctcaccg
241 ccgttgaaca gagccaaaag catactcgct tgcttaaacg cattcgaacc aatatgtgca
301 gccgcaaacc cagcagaccc gaaccggttc ctccantgac ttcaacgttt catgacggtt
361 caacttcggt ca
```

FIG.28A-2

```
    ttttttttta agtgagaacc ttaacaaatt taaccatttg aactgaaata tgaacatgta
 61 aagactcatt cacacttagc aaataggttt agaaccaaaa ctctaattat ttttatataa
121 tagggaaaaa aaagaaagaa aaattcttcc ataagtgtta gattagcttt tagtacctgt
181 gatcacccct aacctctggt aataatacat ggagatgatt taaccagtta cacaataacc
241 caagattaca gtaaaaacat aattatgttt tatgaaacat aaagactata tgctcttgtc
301 acttatctta cctccaagct gaagcaacgg attaagcttt tctcctccca gcaaaaatgg
361 gagctcaccc atttcttctt taaggttgta cttnttgca
```

FIG.28A-3

```
    gctatggaag gagagaagat ggttcatgtg attgatctcg atgcttctga gccagctcaa
 61 tggcttgctt tgcttcaagc ttttaactct aggcctgaag gtccacctca tttgagaatc
121 actggtgttc atcaccagaa ggaagtgctt gaacaaatgg ctcatagact cattgaggaa
181 gcagagaaac tcgatatccc gtttcagttt aatcccgttg tgagtaggtt agactgttta
241 aatgtagnac agtttagggt ttaaacagga gaggcnttag ccgttagctc ggttcttcaa
301 ttgcata
```

FIG.28A-4

```
    ccgatcatca aattagttat cttcagctca aattggattt ggtttggtat tacacccaca
 61 ccagaccaaa ttgaaccaac acacaaaggc tttacatgca gaggcagtag aagcatttaa
121 gccaaaatag cataaagaga cagaaagtca ccatcacaaa acaactaaga ttgtgtcccc
181 atgtatacaa aaaagaaagg gactctgctc ataaccaaaa tagaagacaa actgtaatat
241 atcattcact tcctgcatct ccaagctgat accgagtata gaggtcgatc ttgccagcaa
301 attactgcgc acccgntctc ttccttgatt ctatacccat caaaa
```

FIG.28A-5

```
    ctggaattac aattacagca atttgtattc aattgttgaa tctaagcctg gcttcatctc
 61 tttggcctgg aacgatttac ctctcctcac tctttcttcc tggcgataac caaaccaaac
121 cgatccggta ttcttagttt tgttttgttt tcaatgttat ttttggttag acaaatattc
181 aattgttaat atactccgtg gtcagagtgt tttgtttttc ttttagttcg aacgttgaat
241 taattcaggg gtaggttttg aattctctga accttatgtg ttttttggta acatcatttg
301 gatttgtgaa ctaggtttaa aaactggtct tagtcttgtt gttttctcat tagataattt
361 aaactggttt gcttctttat ttttgggttg ggataaaagt gaccgg
```

FIG.28A-6

```
    gtggaattac aattacagca atttgtattc aattgttgaa tctaagcctg gcttcatctc
 61 tttggcctgg aacgatttac ctctcctcac tctttcttcc tggcgataac caaaccaaac
121 cgatccggta ttcttagttt ttgttttgtt ttcaatgtta tttttggtta gacaaatatt
181 caattgttaa tatactccgt ggtcagagtg ttttgttttn cttttagttc gaacgttgaa
241 ttaattcagg ggtaggtttt gaattctctg aacctnatgt gttttntggt aacatcattt
301 ggatttgtga actaggttta aaaactggnc ttagtcttgt tgttttctca ttaggataat
361 ttaaactggt ttgcttcttt attttnggtt gggataaagt gaccgg
```

FIG.28A-7

caaaactaca tttcatcact tttttgagca aaattacaaa taaaagagta gttacaaata
61 tatttggctt tcaacttcct aattttatga aatagtaatt acatctcaaa cagatgacca
121 gaaccggtca ctttatccaa ccaaaaataa agaagcaaac cagtttaaat tatctaatga
181 gaaaacaaca agactaagac cagtttttaa acctagttca caaatccaaa tgatgttacc
241 aaaaaacaca taaggttcag agaattcaaa acctacccct ganttaattc aacgttcgaa
301 ctaaaagaaa aacaaaacac tctgaccacg gagtatatta acatttgatt atttgtctaa
361 ccaaaaataa cattgaaaac aaaacaaaac tanggaatac cggatcggt

FIG.28A-8

cccaacgggt cctgagcttc ttacttatat gcatatcttg tatgaagcct gcccttattt
61 caaattcggt tatgaatctg ctaatggagc tatagctgaa gctgtgaaga acgaaagttt
121 tgtgcacatt atcgatttcc agatttctca aggtggtcaa tgggtgagtt tgatccgtgc
181 tcttggtgct agacctggtg gacctccgaa cgttaggata acgggaattg atgatccgag
241 atcatcgttt gctcgtcaag gaggacttgc agttagttgc acaaagcact tggca

FIG.28A-9

gggtcatcaa catatcactt actactacaa catttgacaa cttgttcctn cggatcatgc
61 atgagtttta cttttacaaa cagattctgc aaactttaaa agcaagtttc taatctcttc
121 tgaaaccgaa caaggttttt attagttacc tccaagcaca agaagtgata agaggttgat
181 tcttccatcc taaatacaat gctccatctc tttcttcaag tgtatacttc tctgaataac
241 tctcaagcaa tcctttgatt gttgcgttca catacgagct caaaggatac ggtttaaatc
301 ccgccatgtg aaaccgaga

FIG.28A-10

caaaaattta tatatttgtg tgaacttaaa tttaaaaatc catcgcactg agcaaaataa
61 nntcagaaac taaaaatttg tcatttaaga taaattgaat taaggaaaat atttttttaa
121 taattgaaac tccggtggaa atcaggagga gcgacatctc catgctgaaa ctccgacgag
181 ttctgtcctt tgccaacata ggagaagtga gttatgtttc tcctcgacgt gaaagcctct
241 cactggcgtc cgttggntna aacactcggc ttgagactcc gtgaagttac tgtgcgtcac
301 cggtgagaaa cccatctgta gaaacatcgc ttgccacgtc atcatcggcc tttctatcgg
361 acggctacga tccaacacca gcttctctat ctccggctgt ataaggaaa

FIG.28A-11

```
    ctattttnac aatttatttt gttattagaa gtggtagtgg agtgaaaaaa caaatcctaa
 61 gcagtcctaa ccgatccccg aagctaaaga ttctncacct tcccaaataa agcaaaacct
121 agatccgaca ttgaaggaaa aacctttag atccatctct gaaaaaaacc aaccatgaag
181 agagatcatc atcatcatca tcatcaagat aagaagacta tgatgatgaa tgaagaagnc
241 gacggtaacg gcatggatga gcttctagct gttcttggtt ataaggttag gtcatccgaa
301 atggctgatg tttgctcaga aactcgagca gcttgaagtt atgatgtcta atgttcaagn
361 aagncggtct ttntcaactt cgcnacttnn gactgttcac tntaatncgg cggnngtttt
421 caacgntggc ttgntttcna tgntnaccga ccttaat
```

FIG.28A-12

```
    atgggaaagg agcatttaat ctcgactcaa ttgctctacg agctctctcc ttgtttcaaa
 61 ctcggtttcg aggccgcgaa tctcgccatt ntcgacgccg ccgataacaa cgacggtgga
121 atnatgatac cgcacgtaat cgatttcaat atcggagaag gtggacaata cgttaacctt
181 ctccntacat tatccacgcg ccggaatggt aaaagtnaga gtcagaattc tccggtggtt
241 aanatcaccc gccgtggcga acaacgttta cgggatgttt agtcggatga cgggtggnga
301 agagaggttt aaaagcccgt ncgngntttt ttttgnagcc actncngntn atccg
```

FIG.28A-13

```
    actcggtatc tccgtaagtt tcaacgtggt gacgagttta cgactcggtg atctgaatcg
 61 tnaatctntc gggtgtnatc ccgacgagac tttggctgta aacttagctt tcaagcttta
121 tcgtgttccc gacgaaagcg tatncacgga gaatccaaga cgaacttctc cggcgcgtga
181 agggacttaa accgcgcgtg gttactctag tggagcaaga aatgaattcg aatacggcgc
241 cgtttttagg gagagtaagt nagtcatgcg cgtttnacgg tgcgttnctt gantcggtcg
301 agtctacggt tcctagtacg gatttccgac ccgtgccaaa atttnnggaa ggaatttgcc
361 cgnaannttn naaaccgggt g
```

FIG.28A-14

```
    atnaaaagtc ttttttttt ctttgttaca taagattcct acacttttcg aaatggaaaa
 61 tcacaatgat aataatatca gaataatctc gaaaattaat aataatatgg taataataag
121 aagaaaaaaa aagagtgtgt gaagttaacg ccaagcggat gcgacagtga gtgcccgtcc
181 catccaacca aagcacacac ctccgttatc ttctttaacg gtaaagcccg ggtggactcg
241 gtttccacga ctcttcatcg actccgctat cttctcactc aatggcatta actcaaaccc
301 agccatgctc atccgcattc gccatttncc ggaacanctc gnaccgctct atacgntcga
361 ttccttcgga cggcaccgng ttttactagc ttccggncaa ttccttcctn aactttggaa
421 cggtnggatt cgttcttggg accgtaggct tggcccgctt aagaacgnac cgtacagggg
481 nntgttttnt taatttccct taaaaggggg cgntttggg ttnatttttn ana
```

FIG.28A-15

```
    caaccntttt atagtcaagc agctctcaac gctttttttt caaggtctgt naagcctcga
 61 aattatcaga ntttncaatc tccgtcgccg atgattganc tcacgtcggt gaatgatatg
121 agtttntttg gnggttctgg ttcatctcag cnttacggtt taccggttcc caggtctcan
181 acgcaacagc aacaatcgga ttacggttta tttggtggga tccgaatggg aatcgggtcg
241 ggtattaata attatccaac attaaccggc gttccgtgta ttgaaccggt tcaaaaccgg
301 gttcatgaat cggaggacca ttgttganta agnttaagag agctttgtng aaacaanctt
361 tttangattg atnaccg
```

FIG.28A-16

```
    tgcatacaac gcaccgtttt tcgtaacacg gtttcgcgaa gtctatttca tttctcctcg
 61 atttttgaca tgcttgagac aattgtgcca cgagaagacg aagagaggat gttccttgag
121 atggaggtct ttgggagaga ggcactgaat gtaattgctt gcnaaggttg ggaaagagtg
181 gagaggcctg agacatacaa gcagtggcac gtacgggcta tgaggtcagg gttggtgcag
241 gttccatttg acccaagcat tatgaagaca tcgctgcata aggtccacac attctaccac
301 aaggattttg tgatcggtca aagataaccg ggtggctctt tcaaggntgg aaggggaagg
361 anctgtcatg ggtctttctt ttttggaaac cagagtccca aggttttncc ggaaaatcct
421 ccttgggnat ttnangnccc tttttttgtt tttttncccn gnnanttccc nggggnagtt
481 tccagtttna ggngngtttt tncnaaaa
```

FIG.28A-17

```
    tgcatacaac gcaccgtttt tngtaacacg gtttcgcgaa gtctatttna tttctcctcg
 61 atttttgaca tgcttganac aattgtncca cgagaagacg aagagaggat gttccttgan
121 atggaggtct ttgggagana ggcactgaat gtaattnctt gcnaaggttg ggaaagagtg
181 gagaggcctg anacatacaa gcagtggcac gtacgggcta tgaggtcagg gttggtgcag
241 gttccatttg acccaagcat tatgaagaca tcgctgcata aggtccacac attctaccac
301 aagggttttt tgatccntcc aagataaccg gtggctcttn caaagctttg aagggaagga
361 cctttcatgg gtcttttctt ttttggaacc aggtcccaag gttttncccg gaatccccgn
421 tggaattttg nnnccccttt tgatttttt tccccggnaa ttnccc
```

FIG.28A-18

```
    gagacggtag atccgncgcg ctaaagcttc ggcgaagtaa gtagccactt tnntnatagc
 61 tccggcttga nacacagcta agcatccnat ttgcttcaca agagcttccg ctagagtcaa
121 attgtnctnc tggattgctt ctgcacaagc cataagcgcg tggactaaac gaacaccgtt
181 ctcttgcgag tnaaccagga taacagaacg anttgactca gccgccgccg tcgttgtcgt
241 ggtggttgtc gtcaccgtcg ttcctatgac tccaccaatn tgggtacccg tcgaagtcga
301 tgtaaccata ggatcagggc ttcgngcatg nttttaaaac gg
```

FIG.28A-19

```
    gtttgattcg ttggaaggag ttccgaatag tcaagacaaa gtcatntctg aagtttactt
  61 agggaaacag atttgtaatc nggtggcttg tnaagntcct gacagagtcg agagacacga
 121 aacgttgagt caatngggaa accggtttgg ttcgtccggt ttagcgccgg cacatcttgg
 181 gtctaacgcg tttaagcaag cnagtatnct tttntntgtn tttaatagtg gccaaggtta
 241 tcgtgtggag gagagtaatg gatgtttgat gttgggttgg cacactnngc ccactcattt
 301 accacctccg gttttggaaa c
```

FIG.28A-20

```
    taaaaattga tcccaaaaag gcataaatta aaaatgacct accaaaacga tatatataag
  61 aattttaaac aagtgaacga aaataaataa aataaacaaa aggcaaaacg gttcgattca
 121 gttcggttta ggtcttggtc cgaacatatg tcatcaccgg tccactgatc tcaatctcaa
 181 attcactcgn ctcgactcca ccaccgtcgt atgcttcgag tcaaactcag tacgncgccg
 241 tcgagagttt ccaagcggag gtggtaatga gtggacgagt gtgccaaccc ancatcaaac
 301 atccattact ttcctccaca cgntaacctt ggccactatt taaacacagg caaaangcat
 361 acttgtttgc ttaaaccgcg ttagnccnaa gntttgccgg gcgntaaacc cggcngaccc
 421 aanccggntt tcccnatttg ctcaaacggt ttngtgnctt ttggcttttt gnatggcctt
 481 taaangnncc
```

FIG.28A-21

```
    aaaaaatggg aaaccatcac tcttgatgaa cttatgatca atccaggaga gacaacggtc
  61 gtcaacngca ttcatcggtt acaatacacn cctgatgaaa ctgtgtcatt agactctcca
 121 agagacacgg ttctgaagct attcagagat atcaatcctg acctctttgt gtttgcagag
 181 attaacggaa tgtacaactc tcctttcttc atgacgaggt tccgagaagc gcttttncat
 241 tacncttcac tctttgacat gtttgacacc acaatacacg gagaggatga gtacaaaaac
 301 aggtcactgt ttggagagag agttactttt gaganacgcg nttgagcgtg attttcctgc
 361 nngggnttca nancgggttt tnngggcctt aaaacctnca agaaatnggn ggtttgggtt
 421 tt
```

FIG.28A-22

```
    aatcaatgtt ttggttatat ttcattacta gcaacccacc cacaaccaca tgacaattta
  61 caagagaaaa acaaccacca ggtttggttt gtatacatat ataacttagg ttgtgttaca
 121 acttaaaaca tcattgcaca tcctaaaaat ttcagcgacc agaatgtgtt tttgattgtg
 181 cctctttctt tatccacctc aagtaaccat cattcactat aacttaccca atct
```

FIG.28A-23

```
    gcgaatgttg agatcttgga agcaatagct ggggaaacca gagtccacat tatcgatttt
 61 aagattgcac agggatcaca atacatgttt ttaattcagg agcttgcgaa acgccctggt
121 gggccgccgt tgctgcgtgt nacgggtgtg gatgattcan agtccaccta tgctcgtggg
181 ggaggactca gcttggtagg tgagaggctt gcaactttgg cgcagtcatg tggtgtcccg
241 tttnagtttc acgatgccat catgtctggg tgcaaggtgc agcgggaaca tctcgggttg
301 gaacctggct ttgctgttgt tgtgaacttc ccatatgtat tacaccacat gccagacgag
361 agcgtaagtt tttgaaaatc acagngacag gcttctgcat ctnatcaana gcctttcccc
421 aaactggtac tctagtaggc aagattcaac acaacacttg catcna
```

FIG.28A-24

```
    atgnaacata tagcaaaaga tcatgcaatg agtactatat ctcttaggct acactcttac
 61 acacgctatg tcacaagcat aatataacaa cattctagtg ttcaagaacc ctaactctga
121 acttaatcca ctcgtgttgg cgagagacta tcaacagaaa agccctacat aaatcccagt
181 cgcttagaac gtaaganaca acatctatga agacgaagga acccatagag atgaagcata
241 cacgattcta cctttccacc cttgaagtaa ccagttaccg ttttgatcaa catcgaagtt
301 tttatcgtac ccgttttcgg attttcaact tcagattctg catcagttcc ttctcaagcg
361 gnagctgtcc taaatccggg tcgggtcagt ctcggctggc actggttata tggctctggg
421 ctctccactc tctctggtct tcacaaggca cancattcac aatctntttt ccataaaact
481 nnttttcntn catnngncnn atnttggctt ccctnggntg gttggggnnc ncnt
```

FIG.28A-25

```
    tcaaggttct tctttgtcat cttgttgccg aatccacaaa gaggagaata aagattcgac
 61 ctttattaga tattaacgac tctggatttt tgggtttttg gagttggatc cacatgggtt
121 cttatccgga tggattccct ggatccatgg acgagttgga tttcaataag gactttgatt
181 tgcctccctc ctcaaaccaa accttaggtt tagctaatgg gttctattta gatgacttag
241 atttctcatc cttggatcct ccagaggcat atccctccca gaacaacanc aacaacatca
301 tcaacaacaa agctgtagca ggagatctgt tatcatcttc aactgaatga cgntggattc
361 tctgattctg ttttgagtat ataagccaag ttctnatggg agnnggtnat gnagagaagc
421 ctttgtatgt tcatgnngnt ttggtnatta agntgctngg aaannactcn ntnngc
```

FIG.28A-26

```
LSMVNELRQI VSIQGDPSQR IAAYMVEGLA ARMAASGKFI YRALKCKEPP
SDERLAAMQV LFEVCPCFKF GFLAANGAIL EAIKGEEEVH IIDFDINQGN
QYMTLIRSIA ELPGKRPRLR LTGIDDPESV QRSIGGLRII GLRLEQLAED
NGVSFKFKAM PSKTSIVSPS TLGCKPGETL IVNFAFQLHH MPDESVTTVN
QRDELLHMVK SLNPKLVTVV EQDVNTNTSP FFPRFIEAYE YYSAVFESLD
MTLPRESQER MNVERQCLAR DIVNIVACEG EERIERYEAA GKWRARMMMA
GFNPKPMSAK VTNNIQNLIK QQYCNKYKLK EEMGELHFCW EEKSLIVASA
WR*
```

FIG.28A-27

AMEGEKMVHV IDLDASEPAQ WLALLQAFNS RPEGPPHLRI TGVHHQKEVL
EQMAHRLIEE AEKLDIPFQF NPVVSRLDCL NVEQLRVKTG EALAVSSVLQ
LHTFLASDDD LMRKNCALRF HNNPSGVDLQ RVLMMSHGSA AEARENDMSN
NNGYSPSGDS ASSLPLPSSG RTDSFLNAIW GLSPKVMVVT EQDSDHNGST
LMERLLESLY TYAALFDCLE TKVPRTSQDR IKVEKMLFGE EIKNIISCEG
FERRERHEKL EKWSQRIDLA GFGMVPLSYY AMLQARRLLQ GCGFDGYRIK
EESGCAVICW QDRPLYSVSA WRCRK*

FIG.28A-28

GTSPTGPELL TYMHILYEAC PYFKFGYESA NGAIAEAVKN ESFVHIIDFQ
ISQGGQWVSL IRALGARPGG PPNVRITGID DPRSSFARQG GLELVGQRLG
KLAEMCGVPF EFHGAALFCT EVEIEKLGVR NGEALAVNFP LVLHHMPDES
VTVENHRDRL LRLVKHLSPN VVTLVEQEAN TNTAPFLPRF VETMNHYLAV
FESIDVKLAR DHKERINVEQ HCLAREVENL IACEGVEREE RHEPLGKWRS
RFHMAGFKPY PLSSYVNATI KGLLESYSEK YTLEERDGAL YLGWKNQPLI
TSCAWR*

FIG.28A-29

AAIFYGHHHH TPPPAKRLNP GPVGITEQLV KAAEVIESDT CLAQGILARL
NQQLSSPVGK PLERAAFYFK EALNNLLHNV SQTLNPYSLI FKIAAYKSFS
EISPVLQFAN FTSNQALLES FHGFHRLHII DFDIGYGGQW ASLMQELVLR
DNAAPLSLKI TVFASPANHD QLELGFTQDN LKHFASEINI SLDIQVLSLD
LLGSISWPNS SEKEAVAVNI SAASFSHLPL VLRFVKHLSP TIIVCSDRGC
ERTDLPFSQQ LAHSLHSHTA LFESLDAVNA NLDAMQKIER FLIQPEIEKL
VLDRSRPIER PMMTWQAMFL QMGFSPVTHS NFTESQAECL VQRTPVRGFH
VEKKHNSLLL CWQRTELVGV SAWRCRSS*

FIG.28A-30

KKWETITLDE LMINPGETTV VNCIHRLQYT PDETVSLDSP RDTVLKLFRD
INPDLFVFAE INGMYNSPFF MTRFREALFH YSSLFDMFDT TIHCERRDEV
ISCEGAERFA RPETYKQWRV RILRAGFKPA TISKQIMKEA KEIVRKRYHR
DFVIDSDNNW MLQGWKGRVI YAFSCWKPAE KFTNNNLNI*

FIG.28A-31

ANVEILEAIA GETRVHIIDF QIAQGSQYMF LIQELAKRPG GPPLLRVTGV
DDSQSTYARG GGLSLVGERL ATLAQSCGVP FEFHDAIMSG CKVQREHLGL
EPGFAVVVNF PYVLHHMPDE SVSVEKYRDR LLHLIKSLSP KLVTLVEQES
NTNTSPLVSR FVETLDYYTA MFESIDAARP RDDKQRISAE QHCVARDIVN
MIACEESERV ERHEVLGKWR VRMMMAGFTG WPVSTSAAFA ASEMLKAYDK
NYKLGGHEGA LYLFWKRRPM ATCSVWKPNP NYIG*

FIG.28A-32

LLKVLLCHLV AESTKRRIKI RPLLDINDSG FLGFWSWIHM GSYPDGFPGS
MDELDFNKDF DLPPSSNQTL GLANGFYLDD LDFSSLDPPE AYPSQNNNNN
NINNKAVAGD LLSSSSDDAD FSDSVLKYIS QVLMEEDMEE KPCMFHDALA
LQAAEKSLYE ALGEKDPSSS SASSVDHPER LASHSPDGSC SGGAFSDYAS
TTTTTSSDSH WSVDGLENRP SWLHTPMPSN FVFQSTSRSN SVTGGGGGGN
SAVYGSGFGD DLVSNMFKDD ELAMQFKKGV EEASKFLPKS SQLFIDVDSY
IPMNSGSKEN GSEVFVKTEK KDETEHHHHH SYAPPPNRLT GKKSHWRDED
EDFVEERSNK QSAVYVEESE LSEMFDNMFL CGPGKPVCIL NQNFPTESAK
VVTAQSNGAK IRGKKSTSTS HSNDSKKETA DLRTLLVLCA QAVSVDDRRT
ANVXLRQIRE HSSPLGNGSE RLAHYFANSL EARLAGTGTQ IYTALSSKKT
SAADMLKAYQ TYMSVCPFKK AAIIFANHSM MRFTANANTI HIIDFGISYG
FQWPALIHRL SLSRPGGSPK LRITGIELPQ RGFRPAEEFR RQVIAWLDTV
SDTMFRLSTT QLLRNGETIQ VEDLKLRQGE YVVVNSLFRF RNLLDETVLV
NSPRDAVLKL IRKINPNVFI PAILSGNYNA PFFVTRFREA LFHYSAVFDM
CDSKLAREDE MRLMYVFEFY GREIVNVVAS EGTERVESRE TYKQWQARLI
RAGFRQLPLE KELMQNLKLK IENGYDKNFD VDQNGNWLLQ GWKGRIVYAS
SLWVPSSS*

FIG.28A-33

```
                |-------------------- LEUCINE HEPTAD I -----------------|
                |---------- A ------------|              |------ B -------|
SCL9    EVVDLRSLLIHCAQAVAADDRRCAGQLLKQIRLHSTPF-GDGNQRLAHCFANGLEARLAGTGSQIYKGT/SKP----RSAAAVLKA
SCL14   ETADLRTLLVLCAQAVSVDDRRTANVKLRQIREHSSPL-GNGSERLAHYFANSLEARLAGTGTQIYTALSSKK----TSAADMLKA
SCL1                          LSMVNELRQIVSIQ-GDPSQRLAAYMVEGLAARMAASGKFIYRALKCKE----PPSDERLAA
SCL8    TSVCSRQTVMEIATAIAEGKTEIATEILARVSQTPNLE-RNSEEKLVDFMVAALRSRIASPVTELY----GKE---------HLIS
SCL4    FDLEPPLLKAIYDCARISDSDPNEASKTLLQIRESVSELGDPTERVAFYFTEALSNRLSPNSPA--------TSSSSSSTEDLILS
SCL6    GPVGITEQLVKAAE-VIESDTCLAQGILARLNQQLSSPVGKPLERAAFYFKEALNNLLHNVSQT----------LNPYSLIFKIAA
SCL15   GGFGFIEDLIRVVDCVESDELQLAQVVLSRLNQRLRSPAGRPLQRAAFYFKEALGSFLTGSNRN------PIRLSSWSEIVQRIRA
SCL18   AQNLLSILSLNSSPHGDSTERLVHLFTKALSVRINRQQQDQTAETVATWTTNEMTMSNSTVFTSSVCKEQFLFRTKNNNSDFESCY
GAI     NGVRLVHALLACAEAVQKENLTVAEALVKQIGFLAVSQIG-AMRQVATYFAEALARRIYRLSPS----------QSPIDHCLSDTL
RGA     NGVRLVHALMACAEAIQQNNLTLAEALVKQIGCLAVSQAG-AMRKVATYFAEALARRIYRLSPP----------QNQIDHSLSDTL
RGAL    TGVRLVHALLACAEAVQQNNLKLADALVKHVGLLASSQAG-AMRKVATYFAEGLARRIYRIYPR----------DDVASSSFSDTL
SCR     EGLHLLTLLLQCAEAVSADNLEEANKLLLEISQ-LSTPYGTSAQRVAAYFSEAMSARLLNSCLGIYAALPSRW-MPQTHSLKMVSA

                |------------------------------ VHIID -------------------------------|
SCL3                                AMEGEKM----VHVIDLDASEPAQWLALLQAFNSRPEG------PPHLRITGVHHQ-----
SCL9    HQLFLACCPFRKLSYFITNKTIRDLVGNSQR----VHVIDFGILYGFQWPTLIHRFSMYG--------SPKVRITGIEFPQPGFR
SCL14   YQTYMSVCPFKKAAIIFANHSMMRFTANANT----IHIIDFGISYGFQWPALIHRLSLSRPGG-----SPKLRITGIELPQRGFR
SCL16   LAEFVDLTPWHRFGFIAANAAILDAVEGYSS----VHIVDLSLTHCMQIPTLIDSMANKLHKKP----PPLLKLTVIASDAEFHP
SCL13                     ANVEILEAIAGETR----VHIIDFQIAQGSQYMFLIQELAKRPGG------PPLLRVTGVDDSQSRYA
SCL5    MHILYEACPYFKFGYESANGAIAEAVKNESF----VHIIDFQISQGGQWVSLIRALGARPGG------PPNVRITGIDDPRSSFA
SCL1    MQVLFEVCPCFKFGFLAANGAILEAIKGEEE----VHIIDFDINQGNQYMTLIRSIAELPGK------RPRLRLTGIDDPESVQR
SCL8    TQLLYELSPCFKLGFEAANLAILDAADNNDGGMMIPHVIDFDIGEGGQYVNLLRTLSTRRNGKSQSQNSPVVKITAVANNVYGCL
SCL4    YKTLNDACPYSKFAHLTANQAILEATEKSNK----IHIVDFGIVQGIQWPALLQALATRTSGK-----PTQIRVSGIPAPSLG--
SCL6    YKSFSEISPVLQFANFTSNQALLESFHGFHR----LHIIDFDIGYGGQWASLMQELVLRDNAA-----PLSLKITVFASPA----
SCL15   IKEYSGISPIPLFSHFTANQAILDSLSSQSSSPF-VHVVDFEIGFGGQYASLMREITEKSVS------GGFLRVTAVVA------
SCL18   YLWLNQLTPFIRFGHLTANQAILDATETNDNGA--LHILDLDISQGLQWPPLMQALAERSSNPSSP--PPSLRITGCGRDVTGL-
GAI     QMHFYETCPYLKFAHFTANQAILEAFQGKKR----VHVIDFSMSQGLQWPALMQALALRPGG------PPVFRLTGIGPPA----
RGA     QMHFYETCPYLKFAHFTANQAILEAFEGKKR----VHVIDFSMNQGLQWPALMQALALREGG------PPTFRLTGIGPPA----
RGAL    QIHFYESCPYLKFAHFTANQAILEVFATAEK----VHVIDLGLNHGLQWPALIQALALRPNG------PPDFRLTGI--------
SCR     FQVFNGISPLVKFSHFTANQAIQEAFEKEDS----VHIIDLDIMQGLQWPGLFHILASRPGG------PPHVRLTGLGTSM----
```

FIG.29A

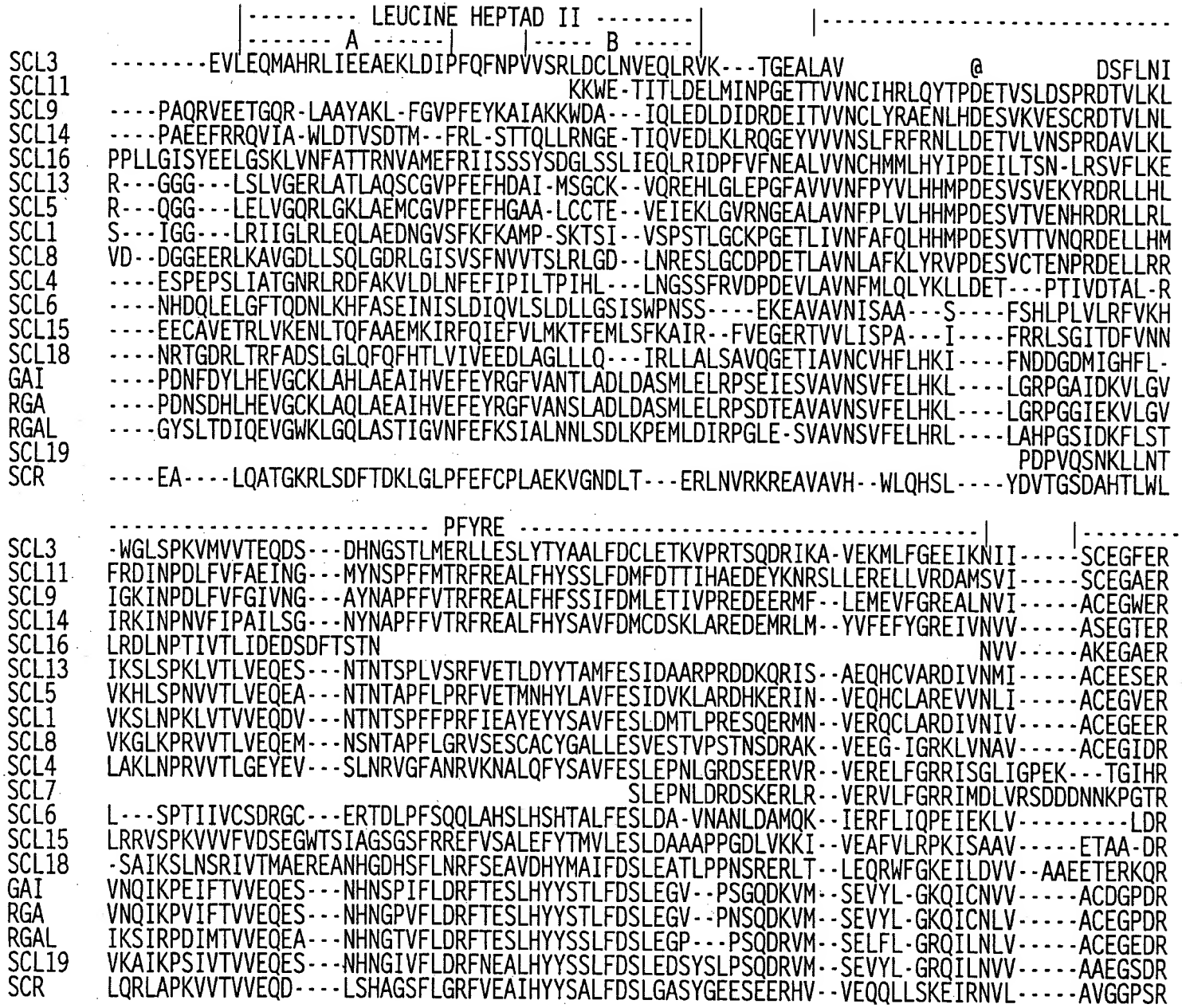


FIG.29B

```
         ------------------------ SAW -------------------------------------|
SCL3     RERHEK-LEKWSQRIDLAGFGNVPLSYYAMLQARRLLQG-CGFDGYR-IKEESGCAVICWQDRPLYSVSAWRCRK
SCL11    FARPET-YKQWRVRILRAGFKPATISKQIMKEAKEIVRK-RYHRDFVI-DSDNNWMLQGWKGRVIYAFSCWKPAEKFTNNNLNI
SCL9     VERPET-YKQWHVRAMRSGLVQVPFDPSIMKTSLHKVHT-FYHKDFVI-DQDNRWLLQGWKGRTVMALSVWKPES
SCL14    VESRET-YKQWQARLIRAGFRQLPLEKELMQNLKLKIEN-GYDKNFDV-DQNGNWLLQGWKGRIVYASSLWVPSSS
SCL16    VERLEP          FTGVGFGETAMTEVKTMLEEHATGWGMKKDVDDDNDVERFVLTWKGHSVMFASAWAPPN
SCL13    VERHEV-LGKWRVRMMMAGFTGWPVSTSAAFAASEMLKA--KNYKL-GGHEGALYLFWKRRPMATCSVWKPNPNYIG
SCL5     EERHEP-LGKWRSRFHMAGFKPYPLSSYVNATIKGLLES--YSEKYTL-EERDGALYLGWKNQPLITSCAWR
SCL1     IERYEA-AGKWRARMMMAGFNPKPMSAKVTNNIQNLIKQ-QYCNKYKL-KEEMGELHFCWEEKSLIVASAWR
SCL8     IERCEV-FGKWRMRMSMAGFELMPLSEKIAESMKSR-GN-RVHPGFTV-KEDNGGVCFGWMGRALTVASAWR
SCL4     ERMEE--KEQWRVLMENAGFESVKLSNYAVSQAKILLWNYNYSNLYSIVESKPGFISLAWNDLPLLTLSSWR
SCL7     FGLMEE-KEQWRVLMEKAGFEPVKPSNYAVSQAKLLLWNYNYSTLYSLVESEPGFISLAWNNVPLLTVSSWR
SCL6     SRPIERPMMTWQAMFLQMGFSPVTHSNFTESQAECLVQR-TPVRGFH-VEKKHNSLLLCWQRTELVGVSAWRCRSS
SCL15    RHTGE---MTWREAFCAAGMRPIQQSQFADFQAECLLEK-AQVRGFH-VAKRQGELVLCWHGRALVATSAWRF
SCL18    HRRFE----IWEEMMKRFGFVNVPIGSFALSQAKLLLRL-HYSEGYN-LQFLNNSLFLGWQNRPLFSVSSW
GAI      VERHET-LSQWRNRFGSAGFAAAHIGSNAFKQASMLLALFNGGEGYR-VEESDGCLMLGWHTRPLIATSAWKLSTN
RGA      VERHET-LSQWGNRFGSSGLAPAHLGSNAFKQASMLLSVFNSGQGYR-VEESNGCLMLGWHTRPLITTSAWKLSTAAY
RGAL     VERHET-LNQWRNRFGLGGFKPVSIGSNAYKQASMLLALYAGADGYN-VEENEGCLLLGWQTRPLIATSAWRINRVE
SCL19    VERHET-AAQWRIRMKSAGFDPIHLGSSAFKQASMLLSLYATGDGYR-VEENDGCLMIRWQTRPLITTSAWKLA
SCR      -SGEVKFESWREKMQQCGFKGISLAGNAATQATLLLGMFP-SDGYTLVDDN-GTLKLGWKDLSLLTASAWTPRS
```

@SSVLQLHTFLASDDDLMRKNCALRFHNNPSGVDLQRVLMMSHGSAAEARENDMSNNNGYSPSGDSASSLPLPSSGRT

FIG.29C

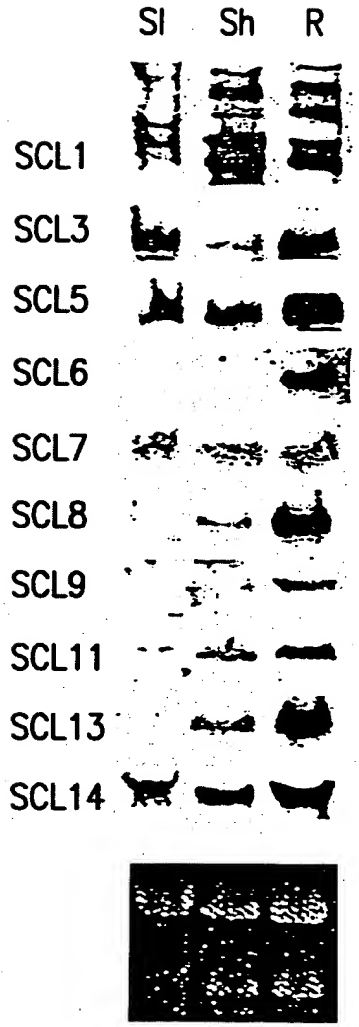


FIG.30

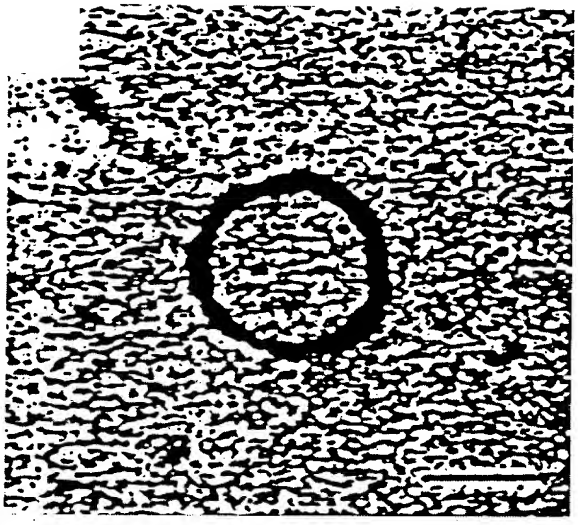


FIG.31A

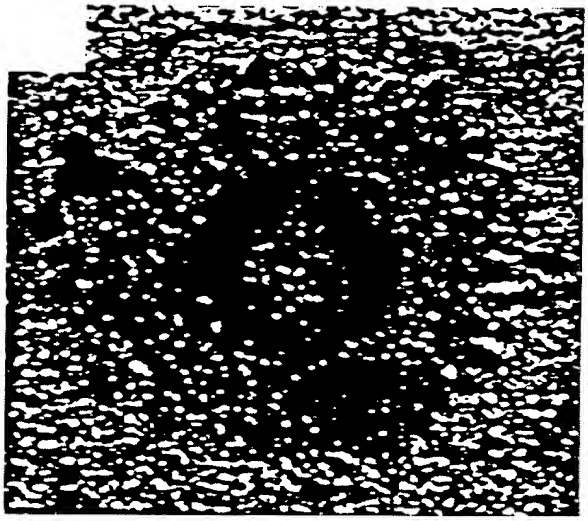


FIG.31B

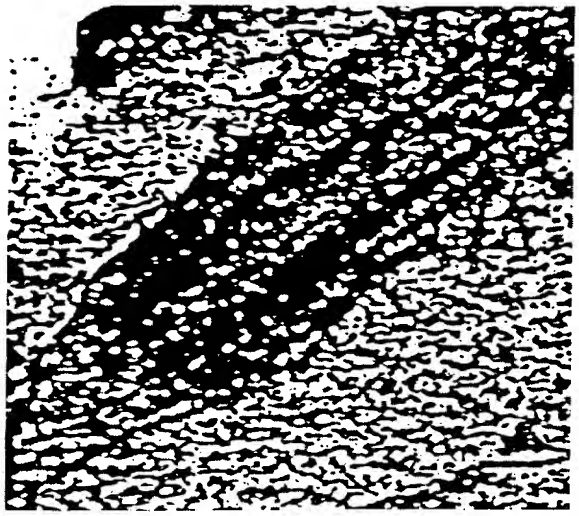


FIG.31C

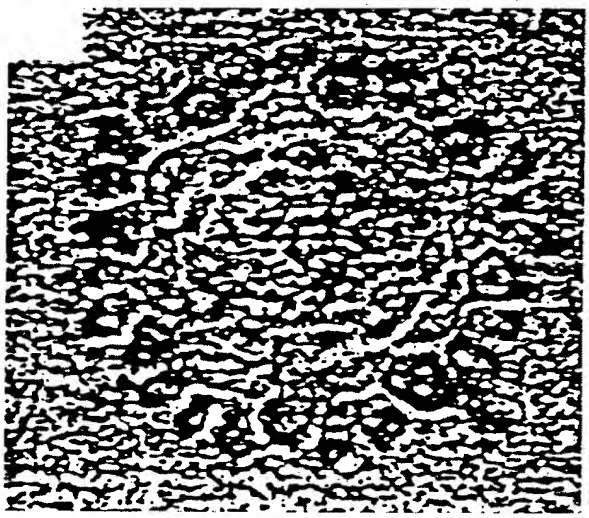
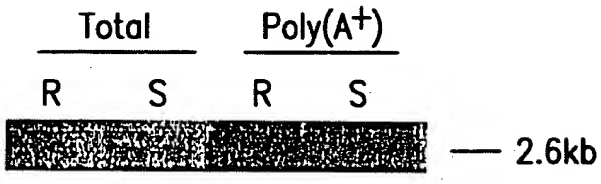


FIG.31D

RNA Blot Analysis



Either total RNA or poly (A+) RNA was probed with the full length of cDNA. About 2.6kb fragment was hybridized to the probe. R: Roots, S: Shoots

FIG.32

CBPBT44 partial cDNA sequence

GCGGCCGCGCAGAGCCGCCGCGTGGCGGTGGCGTTCCAGGCGTACAACGCGCTGTCGCCG
CTCGTCAAGTTCTCGCACTTCACGGCCAACCAGGCCATCCTGCAGGCGCTCGACGGCGAG
GACTGCCTCCACGTGATCGACCTGGACATCATGCAGGGCCTGCAGTGGCCGGGGCTCTTC
CACATCCTCGCGTCCCGCCCGCGCAAGCCGCGGTCGCTCCGGATCACCGGGCTCGGCGCG
TCGCTCGACGTCCTCGAGGCCACTGGCCGCCGCCTCGCCGACTTCGCGGCCTCGCTCGGC
CTCCCGTTCGAGTTCCGCCCCATCGAGGGGAAGATCGGGCACGTCGCCGACGCCGCGGCG
CTCCTCGGCTCGCGCCAGCGGCGGCGGGATGACGAGGCCACCGTGGTGCACTGGATGCAC
CACTGCCTCTATGACGTGACGGGGTCGGACGTGGGCACGGTGCGGCTGCTCCGGAGCCTG
CGCCCGAAGCTGATCACCATCGTGGAGCAGGACCTGGGCCACAGCGGCGATTTCCTGGGC
CGGTTCGTGGAGGCGCTGCACTACTACTCGGCGCTGTTCGACGCGCTGGGAGACGGCGCC
GGCGCGGCCGAGGAGGAGTCGGCCGAGCGGTACGCGGTTGAGCGACAGCTCCTGGGCGCG
GAGATACGCAACATCGTGGCCGTAGGGGGGCCCAAGCGGACAGGGGAGGTGCGCGTGGAG
CGGTGGAGCCACGAACTGCGGCACGCCGGGTTCCGGCCAGTGTCCCTGGCCGGGAGCCCT
GCCGCGCAGGCCAGGCTGCTCCTCGGCATGTATCCGTGGAAGGGGTACACGCTGGTGGAG
GAGGACGCGTGCCTTAAGCTGGGCTGGAAGGACCTCTCCCTGCTCACCGCGTCGGCGTGG
GAGCCGGCGGACGACGCTGCCGCTTCTGCGCCCACCGGTTAACGAGTACGAGCGGACGCG
TGGGTCGAC

FIG.33A

CBPBT44 partial amino acid sequence

AAAQSRRVAVAFQAYNALSPLVKFSHFTANQAILQALDGEDCLHVIDLDIMQGLQWPGLF
HILASRPRKPRSLRITGLGASLDVLEATGRRLADFAASLGLPFEFRPIEGKIGHVADAAA
LLGSRQRRRDDEATVVHWMHHCLYDVTGSDVGTVRLLRSLRPKLITIVEQDLGHSGDFLG
RFVEALHYYSALFDALGDGAGAAEEESAERYAVERQLLGAEIRNIVAVGGPKRTGEVRVE
RWSHELRHAGFRPVSLAGSPAAQARLLLGMYPWKGYTLVEEDACLKLGWKDLSLLTASAW
EPADDAAASAPTGXRVRADAWVD

FIG.33B

```
Zm SCR                                                GRVAAAFQVF NGISPFVKFS
CBPBT44                                               RRVAVAFQAY NALSPLVKFS
At SCR                                                LKMVSAFQVF NGISPLVKFS

Zm SCR  HFTANQAIQE AFEREERVHI IDLDIMQGLQ WPGLFHILAS RPGGPPRVRL
CBPBT44 HFTANQAILQ ALDGEDCLHV IDLDIMQGLQ WPGLFHILAS RPRKPRSLRI
At SCR  HFTANQAIQE AFEKEDSVHI IDLDIMQGLQ WPGLFHILAS RPGGPPHVRL

Zm SCR  TGLGASMEAL EATGKRLSDF ADTLGLPFEF CAVAEKAGNV DPEKLGVTRR
CBPBT44 TGLGASLDVL EATGRRLADF AASLGLPFEF RPIEGKIGHV ADAAALLGSR
At SCR  TGLGTSMEAL QATGKRLSDF TDKLGLPFEF CPLAEKVGNL DTERLNVRKR

Zm SCR  ------EAVA VHWLHHSLYD VTGSDSNTLW LIQRLAPKVV TMVEQDLSHS
CBPBT44 QRRRDDEATV VHWMHHCLYD VTGSDVGTVR LLRSLRPKLI TIVEQDLGHS
At SCR  ------EAVA VHWLQHSLYD VTGSDAHTLW LLQRLAPKVV TVVEQDLSHA

Zm SCR  GSFLARFVEA IHYYSALFDS LDASYGEDSP ERHV---VEQ QLLSREIRNV
CBPBT44 GDFLGRFVEA LHYYSALFDA LGDGAGAAEE ESAERYAVER QLLGAEIRNI
At SCR  GSFLGRFVEA IHYYSALFDS LGASYGEESE ERHV---VEQ QLLSKEIRNV

Zm SCR  LAVGGPARTG DVKFGSWREK LAQSGFRAAS LAGSAAAQAS LLLGMFPSDG
CBPBT44 VAVGGPKRTG EVRVERWSHE LRHAGFRPVS LAGSPAAQAR LLLGMYPWKG
At SCR  LAVGGPSRSG EVKFESWREK MQQCGFKGIS LAGNAATQAT LLLGMFPSDG

Zm SCR  YTLVEENGAL KLGWKDLCLL TASAWRPIQV PPCR
CBPBT44 YTLVEEDACL KLGWKDLSLL TASAWEPADD AAASAPTG
At SCR  YTLVDDNGTL KLGWKDLSLL TASAWTPRS
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FIG.34

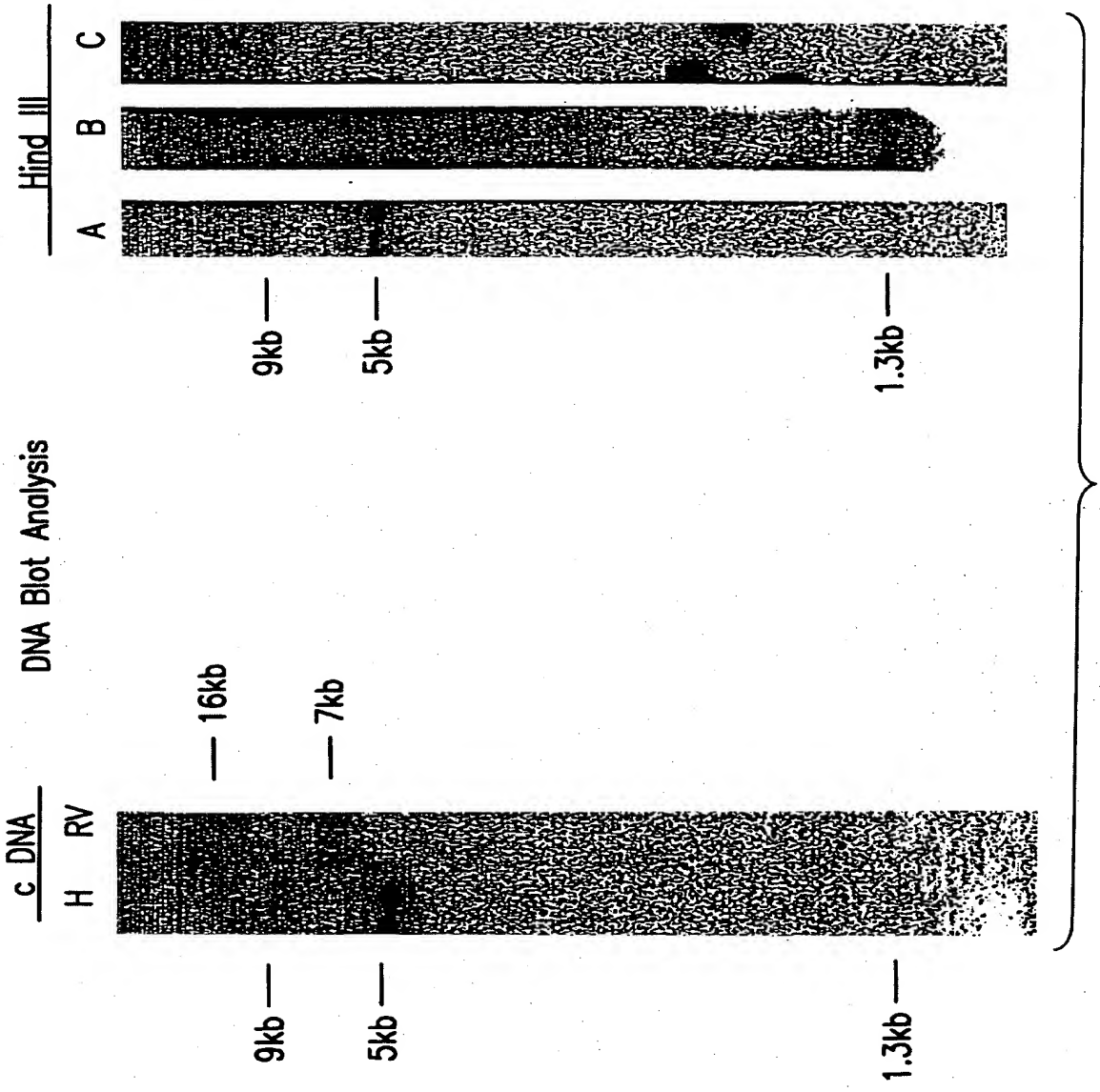

FIG.35